STIC-Biotech/ChemLib

173647

From:

Shaw, Amanda Marie

Sent: To: Wednesday, December 07, 2005 11:54 AM

STIC-Biotech/ChemLib

Subject:

sequence search for 10/713/137

Please search:

1) SEQ ID NO: 2 and 3 (each of these sequences is 24 nucleotides in length). Please limit the search results to nucleic acids that are of a length of 50 nucleotides or less.

2) SEQ ID NO: 1 (258 nucleotides in length)

The CRF has been entered:

http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL_ID=10713137

Please provide a printout of the first 40 results.

Thank you,

Amanda Shaw Patent Examiner Art Unit 1634 Remsen 2E78 Mailbox: REM 2C70 571-272-8668 CREV

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

T	ype of Search
NA#	AA#:
S/L:	Oligomer:
Encode/	Transi:
Structure	#:Text:
Inventor	Litigation:

Vendors and cost where applicable
.STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

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RESULT 1
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258
1 cagcggagtgatggcaagca.....ttgttccccagctgtgcatc 258
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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	ult No.	-	7	٣	4	ហ	9	7	80	0	10	11	12	13	14	15	16	17	18
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ALIGNMENTS

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LOCUS	DO060518 47758 bp DNA linear PRI 23-MAY-2005
DEFINITION	iens nitric oxi
	(NOSZA) gene, complete cds.
ACCESSION	
VERSION	DQ060518.1 GI:66268800
SOURCE	: Homo gapieng (himan)
ORGANISM	
	etazoa:
	Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
REFERENCE	1 (bases 1 to 47758)
AUTHORS	Livingston, R.J., Rieder, M.J., Shaffer, T., Bertucci, C., Baier, C.N.,
	Rajkumar, N., Willa, H.T., Daniels, M., Downing, T.K., Stanaway, I.B.,
	Nguyen, C.P., Gildersleeve, H., Cassidy, C.M., Johnson, E.J.,
	Swanson, J.E., McFarland, I., Yool, B., Park, C. and Nickerson, D.A.
TITLE	Direct Submission
JOURNAL	Submitted (13-MAY-2005) Genome Sciences, University of Washington,
	1705 NE Pacific, Seattle, WA 98195, USA
COMMENT	To cite this work please use: NIEHS-SNPs, Environmental Genome
	Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA
	(URL: http://egp.gs.washington.edu).
FEATURES	Location/Qualifiers
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SLEMSAL"
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422
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                                                                                                                                                              frequency="0.01"
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frequency="0.01"
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/frequency="0.07"
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046
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443
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Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Direct Submission
                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as truns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7: gap of 100 bp
0: contig of 2703 bp in length
0: gap of 100 bp
6: contig of 2076 bp in length
5: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                           contig of 1896 bp in length of 100 bp contig of 989 bp in length of 200 to 200 
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26894: contig of 12028 bp in length
26994: gap of 100 bp
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44060: contigo of 17066 bp in length
44160: gap of 100 bp
116026: contig of 71866 bp in length.
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/clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                         Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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clone_end:SP6
vector_side:left"
1897. _1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                 TITLE
                                                                                                                                                                                               COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21442 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 21501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 ACAGAGTGGAGCCCAGAGGAGACACGCAGCCCGGGCTTACAGACTCACAGGCCCCGTCTT 240
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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Homo sapiens chromosome 17, clone RP11-1145F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC131306
AC131306.1 GI:22325231
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULTOP.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        99.8%; Score 257.6; DB 8 99.6%; Pred. No. 2.3e-49; tive 1; Mismatches 0
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/replace="t"
5002. .5219
/rpt_family="MIR"
/rpt_type=dispersed
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                                                                  /frequency="0.01"
/replace=""
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1 (bases 1 to 116026)
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                                                                                                                                             gene="NOS2A"
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                                      'gene="NOS2A"
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Matches 257; Conservative
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VERSION
KEYWORDS
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Direct Submission

Submitted (109-Aug-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Barnan, B. Musbaum, C., Lender, E., Ali, A., Allen, N., Anderson, S., Barren, B., Musbaum, C., Lender, E., Choepel, Y., Collymore, A., Cooke, P., Dadazaro, B., Choepel, Y., Callymore, A., Cooke, P., Devar, K., Diaz, J. S., Dodge, S., Farreira, P. FitzGerald, M., Gago, D., Galagan, J., Chagaro, B., Horton, L., Hulme, W., Marchen, C., Macdonan, R., Liu, G., Machallano, K., Diaz, J. S., Dodge, S., Kamat, A., Karatas, K., Kali, C., Landers, T., Levine, R., Jones, C., Kamat, A., Karatas, K., Kali, C., Landers, T., Levine, R., Jones, C., Machblad-G., McCarly, M., Machen, J., Meneus, L., Mihova, T., Mengay, V., Murphy, T., Naylor, J., Menger, J., Michhang, P., Pinnkhang, P., Pierre, M., Nachen, J., O'Neil, D., Oilver, J., Peterson, K., Phunkhang, P., Pierre, M., Rayvan, C., Schupback, R., Saaman, S., Severy, P., Roman, J., Young, S., Schupback, R., Saaman, S., Severy, P., Raman, J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

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Is blancan, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

Is blancan, C., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Baguelarkiy, L., Boukhgalter, B., Camarta, J., Chang, J., Matthews, C., McCarthy, M., Manding, J., Matthews, C., McCarthy, M., Manding, J., Matthews, C., McCarthy, M., Manding, J., Match, J., Manding, J., Match, J., Schauer, S., Schauer, S., Terakas, P., Peterson, K., Phunkhang, P., Pierre, J., Peterson, K., Phunkhang, P., Pierre, J., Peterson, K., Phunkhang, P., Pierre, J., Peterson, K., Phunkhang, P., Wajor, J., Peterson, S., T
                                                                                                                                                                                                                                                                                                                                                 Libran, B., Nusbaun, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbaun, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Lindblad-Toh, K., Liudblad-Toh, K., Murchy, Y., Naylor, J., Macdonald, P., Maicor, J., Matchan, C., Norbu, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Zembek, L., Zimmer, A. and Zody, M., Zembek,
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                Hominidae, Homo.

1 (bases 1 to 136599)

Birran, B., Nusbaum, C. and Lander, B.

Homo gapiens chromosome 17, clone RP1-66C13
                                                                                                                                                                                                                                                                                          Unpublished
2 (bases 1 to 136599)
                                            ORGANISM
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Homo sapiens chromosome 17, clone RP1-66C13, complete sequence.
AC130289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7897. .7996
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7997. .9787
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1997. .2985
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12591. .12690
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87934 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                                                                                                                                             / Trp. family="HERN9"

complement (25467. .25477)

/ note="<30 qual SNGL region"

complement (25494. .25499)

/ note="<30 qual SNGL region"

complement (25543. .2551)

/ note="<30 qual SNGL region"

2743. .27546

/ rpt family="LTR12B"

27548 .27637

/ rpt family="LTR30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="MIR"
29297. 29586
/rpt_family="AluSc"
complement(29717. .30006)
/rpt_family="AluSx"
complement(30190. .30319)
/rpt_family="LD"
/rpt_family="LD"
/rpt_family="LD"
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/rpc_family="LIPA5"
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/rpt_family="Aluy"
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20197. .24554
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/rpt_family="L2"
complement(28165.
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                                                                                                                                                                                                                                                                    bonly the first 136.6 kilobases of this clone are being submitted.
The remainder overlaps accession number AC005697 (WICGR project
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Conter project Information
Center project name: L27646
Center clone name: 66_C_13
                                                                                                                                                                                                                                                                                                                                                                                                                      / "GDD="RP1-66C13"
/clone="RP1-66C13"
/clone_lib="RPCI Human PAC library 1"
complement(1. 1738)
/rpt_family="HERVR11"
complement(1739. 2597)
/rpt_family="MER11C"
/rpt_family="MER11C"
3227. .7281
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complement(13628..13920)
/rpt_family="AluSc"
/rpt_family="AluSc"
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16018. 16074
/rpt_family="AT_rich"
complement(16218. 16420)
/rpt_family="LIME4a"
16698. 16723
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2249. 12275
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complement(11241. 11394)
rpt family="Tigger8"
complement(11559. 11864)
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complement (9883, .10013)
rpt family="Alusq"
1199. .11219
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/organism="Homo sapiens"
/-۱ +سمه="qenomic DNA"
                                                                                                                                                                                                                                                                                                                                                                /mol type="genomic DNA
/db_xref="taxon:9606"
/chromosome="17"
/map="17"
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7253 7468
/rpt family="HERVK9"
7484 7913
/rpt family="HERVK9"
8012 . 8930
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8038 . 9389
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/rpt_family="MER9"
9392 . .9652
/rpt_family="AluSq"
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12617. .12907
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complement(13202. .13
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                                                                                                                             Homo sapiens
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                                                        HS66C13 156907 bp DNA linear PRI 17-JUN-2001 Homo sapiens chromosome 17 from PAC RPCI-1 66C13 map 17p11.2 region D178842-D178953, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (28-APR-2000) MOLGENR, Abt Lehrach, Max Planck Institut
But Molekulare Genetik, Ihnestrasse 73, Berlin, 14195 Germany
On Jun 19, 2001 this sequence version replaced gi:13752107.
Clone received from the Resource Centre of the Human Genome Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="17pl1.2"
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/clone lbb="RPCI1,3-5 Human PAC library, originating
instute: Roswell Park Cancer Institute, creator: Pieter
de Jong, P. Ioannou"
/note="region between markers D17S842-D17S953"
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Steffens,C., Klein,M., Heitmann,K., Schuelzchen,S., Starke,A.,
Thompson,C., Radelof,U., Francis,F., Seranski,P., Poustka,A.,
Lehrach,H. and Reinhardt,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     at the Max-Planck-Institute for Molecular Genetics contig 01 1. .156907.
Location/Qualifiers
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156907
/note="T7_end:PAC RPCI-1 66C13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .156907
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome="17"
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                                                                                                            AL354047
AL354047.6 GI:14488115
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                                                                                                                                                           Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                       Unpublished
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Source
                                                                           DEFINITION
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VERSION
KEYWORDS
SOURCE
                                                                                                                                                                          ORGANISM
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AUTHORS
                                             HS66C13/c
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Pasha, A.Q. and Ahsan, A. Method of detecting predisposition to high altitude pulmonary edema Patent: WO 2005047540-A 1 26-MAY-2005; Council of Scientific and Industrial Research (IN) Location/Qualifiers
   PAT 10-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRI 19-AUG-1996
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Submitted (21-MAR-1995) W. Xu, Babraham Institute, MRC Group, Dept
Submitted (21-MAR-1995) W. Xu, BK
Submitted (21-MAR-1995) With that under the acc#X73029.
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Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GACAGAGAGGCCCAGAGAGAACACGCAGGCTTACAGACTCACAGGGCCGGTT
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Molecular clonking and structural organization of the human inducible nitric oxide synthese gene (NOS2)
Biochem. Biophys. Res. Commun. 219 (3), 784-788 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 95.6%; Score 246.6; DB 6; Best Local Similarity 99.2%; Pred. No. 1.7e-46; Matches 257; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
      DNA
CS101221 259 bp DN
Sequence 1 from Patent WO2005047540.
CS101221.1 GI:67509718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .259
/organism="Homo sapiens"
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H.sapiens NOS2 gene, exon 8 and 9.
X85766
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Hominidae, Homo.

Hominidae, Homo.

Hominidae, Homo.

Hominidae, Homo.

Hominidae, Homo.

Homosas 1 to 1152)

Homosas 1 to 1152)

Homosas 1 to 1152)

Homosas 2 to 1152

Homosas 2 
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Submitted (02-MAY-2001) Departamento de Bioquimica, Universidade de Sao Paulo, Rua Professor Lineu Prestes, 748/bloco 12/sala 1200, Sao Paulo, SP 05508-900, Brazil
Location/Qualifiers
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /produčt="nitiric oxide synthase 2A"
/protein id="AAL31486.1"
/db xref="GI:1692453"
/trānslation="YAGYQMPDGSIRGDPANVEFTQ"
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/mol_type="genomic DNA"
/sub_species="chamek"
/db_xref="taxon:118643"
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C1201/25,C12N15/52,G01N33/50,G01N33/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 176.4; DB 8;
Pred. No. 2.4e-30;
1; Mismatches 17;
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BD097464.1 GI:22643038
WO 0166791-A/2.
                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                   /gene="NOS2A"
                                                                                                                                                                                                                                                                                                                                                              <1. .>66
/gene="NOS2A"
                                                                                                                                                                                                                                                                                                                  /gene="NOS2A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 68.4%;
Best Local Similarity 91.2%;
Matches 186; Conservative
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Homo sapiens
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SOURCE
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         JOURNAL
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BD097464
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                                                                               FEATURES
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Ateles belzebuth chamek
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammala; Butheria Buarchontoglires; Primates; Platyrrhini;
Cebidae; Atelinae; Ateles.
1 (bases 1 to 257)
Seuanez,H.N., Lima,C.R., Lemos,B., Bonvicino,C.R., Moreira,M.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Gene assignment in Ateles paniscus chamek (Platyrrhini, Primates).
Allocation of 18 markers of human syntenic groups 1, 2, 7, 14, 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 602;
                                                                                                                                                                                                                                                                                                                                        137. .278
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/product="inducible nitric oxidase synthase"
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/product="inducible nitric oxidase synthase"
/number=9
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/clone lib="PLT6B"
/clone lib="PLT6B"
/clone lib="PLT6B"
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Pred. No. 2.7e-44;
1; Mismatches 13;
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                                       1. .602
/organism="Homo sapiens"
                                                                               /mol_type="genomic_DNA"
/db_xref="taxon:9606"
            Location/Qualifiers
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Best Local Similarity 94.6%;
Matches 244; Conservative
                                                                                                                                                                                                                                                                                                                       /gene="NOS2"
137. .278
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Direct Submission
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/codon_start=1
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nitric oxide synthase.
Homo sapiens (human)
Homo sapiens
46.7%;
  Query Match
Best Local Similarity 99.2
Matches 121; Conservative
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1 (bases 1 to 3462)

1 shii, Y., Ueda, Y., Lwami, M., Arakawa, H. and Not, Y.

1 shii, Y., Ueda, Y., Iwami, M., Arakawa, H. and Not, Y.

1 shii, Y., Ueda, Y., Iwami, M., Arakawa, H. and Not, Y.

1 shii, Y., Ueda, Y., Iwami, M., Arakawa, H. and Not, Y.

1 shiibitors of inducible nitrogen oxide synthetase activation

1 shiibitors of inducible nitrogen oxide synthetase activation 
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C12Q1/25,C12N15/52,G01N33/50,G01N33/15
Method for screening of inhibitors of inducible nitrogen oxide
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10-MAR-2000 JP 00P 72480
YOSHINORI ISHII, YOSHIKO UEDA, MORITA IWAMI, HIROYUKI ARAKAWA, PI
     Method for screening of inhibitors of inducible nitrogen oxide
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                  ice 1. 3462 / Organism='Homo sapiens (human)'. Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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WO 0166791-A/1.
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99.2%;
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Matches 121; Conservative
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FYERPRELEELKWYALPAVAMILLEVGGLEPFGCPFNGWYMGTEIGVRDFCDVQRYNIL
EEVGRRMGLETHKLASLWRQAVVEINIAVLHSFQRQNVTIMDHHSAAESFWKYMQNE
YRSRGGCPADNIAULPOPPHSOSITPVFHQEMLNYVLSPFYYYQYEAWKTHVWQDEKRRP
KRREIPLKYLUKAVLFACKHMRKTWASRVRYTILBYTETGKSEALAMDLGALFSCAFN
FRYCVGMDKYRLSCLEBERLLLAVYTSTFGNGDCPGMGEKLKKSLFMLKELNNKFRYAVF
GLGSSMYRPRCAFADIDQKLSHLGASQLTPMGEGDELSGQBDAFREWAVQTFKAACT
TFDVRGKQHIQIPKLYTSNYTWDPHHYRLVQDSQPLDLSKALSSMHAKNFFRAACT
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/protein id="AAA36375.1"
/bx xref="G1:404049"
/translation="MACPWELFKTKFHQYAMNGEKDINNNVEKAPCATSSPVTQDDL
QYHNLSKQONESPQPLVETGKKSPESLYKLDATPLSSPRHYAIKNWGSGMTFQDTLHH
KAKGILTCRSKSCLGSIMTPKSLTRGPRDKPTPPDELLPQAIEFVNQYYGSFKEAKIE
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Homo sapiens inducible nitric oxide synthase mRNA, complete cds.
L24553
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QYTWILEALDESGSYWVSDKRLPPCELDGALTYFDLDITTPPFOLLLGWAVATEBPER
QRLEALCQPSESSKWKTNBPTELEVLEEPPSLRVSAGFLLSQLPILKPRFYSISSSR
DHTPTEIHLTVAVYYYTRDGGGFPLHGVCSTWLNSLKPQDPVPCFVRNASGFHLED
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EMAQKGVLHAVHTAYSRLPGKPKVYVQDILRQQLASEVLRVLHKEPGHLYVCGDVRMA
RDVAHTLKQLVAAKLKLNEEQVEDYFFQLKSQKRYHEDIFGAVFPYEAKKDRVAVQPS
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TAREMFEHI CRHVRYSTINNGNI RSAI TVFPQRSDGKHDFRVWNAQLI RYAGYQMPDGS
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 3595)
Sherman, P.A., Laubach, V.E., Reep, B.R. and Wood, E.R.
Purification and cDNA sequence of an inducible nitric oxide
synthase from a human tumour cell line
Biochemistry (1993) In press
Original source text: Homo sapiens (library: ATCC ccl221)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Original source text: Homo sapiens (library: ATCC cc1221) colorectal adenocarcinoma cDNA to mRNA.
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0
           Length 3462;
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"Coganism="Homo sapiens"

/mol type="mRNA"

/db xref="taxon:9606"

/db xref="colorectal adenocarcinoma"

/tissue_ltype="colorectal adenocarcinoma"
Score 120.4; DB 6;
Pred. No. 1.2e-17;
0; Mismatches 1;
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HSU20141 3946 bp mRNA linear PRI 12-AUG-1995
Human inducible nitric oxide synthase mRNA, complete cds.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Treatment of viral influenza with antisense oligonucleotides
Patent: WO 0078946-A 2 28-DEC-2000;
Bastern Virginia Medical School (US)
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Pred. No. 1.2e-17;
0; Mismatches 1.
                                                                        Score 120.4; DB 8;
Pred. No. 1.2e-17;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Sequence 2 from Patent WO0078946.
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BELAAVBAVTREIETTVYQLTGDELIFATKQMRARRCIGRIGWSNLQVPDAKSCS
TAREMPEHICHVRYSTRONIRSALTVPPQRSDGKHDFRWMAQLIRVAGVQMPDGS
IRGDPANVEFTQLIRVAGVRRPVYDVALAQANGRDPELFEIPPDLVLEYAMEHP
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ERGRENGRWGLETHKLASLWKDQAVVEINIAVLHSFQKQNVTIMDHHSAAESFWKYMONE
YRRGCPADMIWLYPPPMSGSITPVFHQEMLKYVLSPFYYQVBAWKTHVWQDBKRRP
KRREIPLKVLVKAVLFACMLMRKTMASRVRYTILFATETGKSEALAMDIGALFSCAPN
PKYCYDMYRKLBCLEBERLLLAVYTSFFFGNGPOGPGRGKLKESIPMLKELINNKFRYAVF
GLGSSBYFPRFCAFAHILLAVYTSFFFGNGPOGPGRGKLKESIPMLKELINNKFRYAVF
GLGSSBYFPRFCAFAHILLAVYTSFFRGNGPOGBGRGKAFKSAVGFFKAACF
TFDVRGKQHIQIPKLYTSNVTWDPHYYRLVODSQPLDLSKALSSMAAKNYFTWRLKSR
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QRLEALCOPSEYSKKFTNSPTFLEYLEEPPSLKVSAGFLLSQLPILKERFYSISSPR
DHTPTEIHLTVAVVTYHTROGQELHHGVCSTWLNSLKPQDPVPCFVRNASGFHLPED
PSHPCILIGEGGIAPPRSFWQORLHGSQHKGYRGGRNYTLYFGCRRPDEDHIYOEBN
EMAQKGVLHAVHTAYSRLPGKPKVYYQDILRQQLASEVLRULHKEPGHLYVCGDVRMA
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Human inducible nitric oxide synthase mRNA, complete cds.
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California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0663,
USA
                                                                                                                                                                            1 (bases 1 to 3855)
Maier,R., Bilbe,G., Rediske,J. and Lotz,M.
Maier,R., Bilbe,G., Rediske,J. and Lotz,M.
cloucible nitric oxide synthase from human articular chondrocytes:
cDNA cloning and analysis of mRNA expression
Biochim. Biophys. Acta 1208 (1), 145-150 (1994)
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                   CAGCGGAGTGATGGCAAGGACGTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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      Length 3595;
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Score 120.4; DB {
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="articular chor
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    atch 46.7%;
cal Similarity 99.2%;
121; Conservative
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U05810.1 GI:452487
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      Query Match
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EHLARVEAVTKEIETTGTYQLTGDELIFATKQAWRNAPRCIGRIQWSNLQVFDARSCS
TAREMFEHICRHVRYSTNNGNIRSAITVFPQRSDGKHDFRVWNAQLIRYAGYQMPDGS
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SPROTLIGGGGTGAPFRSFWQQRLHDSGHKGVNGGRATLYFGGRRPDEDHIYOGERN
EMAGKGYLHANHTAYSRLPGRRPKVYVDILASQLASBVLRVLHKEPGHLYVOGDVRMA
RDVAHTLKQLVAAKLKLNBEQVEDYFFQLKSGKRYHEDIFGAVFPYEAKKDRVAVQPS
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QYHNLSKQQNESPQPLVETGKKSPESLVKLDATPLSSPRHVRIKNWGSGMTFQDTLHH
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Hominidae; Homo.
1 (bases 1 to 3946)
Guo,F.H., De Raeve,H.R., Rice,T.W., Stuehr,D.J., Thunnissen,F.B.
                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (20-JAN-1995) Serpil C. Erzurum, Pulmonary & Critical
Care Medicine, Cleveland Clinic Foundation, 9500 Euclid Avenue,
Cleveland, OH 44195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                         Continuous nitric oxide synthesis by inducible nitric oxide synthase in normal human airway epithelium in vivo Proc. Natl. Acad. Sci. U.S.A. 92 (17), 7809-7813 (1995)
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/tissue_type="respiratory epithelium"
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Pred. No. 1.2e-17;
0; Mismatches 1;
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/db_xref="G1:687681"
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/EC_number="1.14.13.39"
/note="inducible isoform"
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Erzurum, S.C.
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15. .347

/EC number="1.14.13.39"

/note="This human inducible NOS possessed consensus

recognition sites for the cofactors FMN, FAD and NADPH and

calmodulin recognition sites."
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/product = inducible type of nitric oxide synthase"
/protein id="BAA0551.1"
/bx xxef = id: 11228940"
/translation="MACPWREFFERTKEHQYAMNGEKDINNNVEKAPCATSSPVTQDDL
QYHNLSKQONESPQPLVETGKKSPESLVKLDATPLSSPRHVRIKNWGSGMTFQDTLHH
ENLARSKSCLGSIMTPKSLTROEDLLPATKGAMSPREFVQYKGSFKRAKIE
EHLARVERYKEATTGTYQLIGDELIFATKQAMSNAPRCIGRIQWEDARSCS
TARREPEHICRHVRYSTNNGNIRSALTVFPQRSDGKHDFRVWNAQLIRYAGYQMPDGS
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PSHPCILIGPGTGIAPFRSFWQRLHDSQHKGVRGGRMTLVFGCRRPDEDHTYQEEM
PROXKGVLHAVHTAYSRLPGKRKVYVQDILRQQLASSVLRVLHKEPGHLYVCGDVRMA
RDVAHTLKQLVAAKLKLNEEQVEDYFPQLKSQKRYHEDIFGAVFPYEAKKDRVAVQPS
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PRI 04-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (18-7AN-1994) Atsushi Hokari, Jikei University School of Medicine, Tokyo, Department of Internal medicine, Division of Gastroenterology and Hepatology; 3-25-8 Nishishimbashi, Minato, Tokyo 105-0003, Japan (E-mail:hokari_a@jikei.ac.jp, Tel:03-3433-1111, Faz:03-3435-0569)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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1 (bases 1 to 3963)
Hokari,A., Zeniya,M. and Esumi,H.
Cloning and functional expression of human inducible nitric oxide synthase (NOS) DNA from a glioblastoma cell line A-172
J. Blochem. 116 (3), 575-581 (1994)
                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
1963 bp mRNA linear PRI 04-OCT-20 HUMITONOS HUMBA for inducible type of nitric oxide synthase, complete
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                                                                                                                                                                                                                    inducible type of nitric oxide synthase; cytokine-related
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/db xref="taxon:9606"
/cell_line="A-172"
/tissue_type="glioblastoma"
/clone_lib="lambda_ZAPII"
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Hokari,A.
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Homo sapiens
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D26525.1 GI:559326
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1 (bases 1 to 4062)
Au-Young, J. and Seilhamer, J.J.
Auchopsition for the detection of signaling pathway gene expression Patent: US 6500938-A 1478 31-DEC-2002;
Incyte Genomics, Inc.; Palo Alto, CA;
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                                                                                             61 GOCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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Patent: EP 1394274-A 155 03-MAR-2004;
Genox Research, Inc. (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Pred. No. 1.2e-17;
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 Pred. No. 1.2e-17;
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Sequence 155 from Patent EP1394274.
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/organism="Homo sapiens"
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CQ776469.1 GI:45379859
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Matches 121; Conservative
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              Matches 121; Conservative
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Patent: EP 1394274-A 38 03-MAR-2004;
Genox Research, Inc. (JP)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 11 from patent US 6171856.
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Sequence 38 from Patent EP1394274.
CQ776352 CQ776352.1 GI:45379742
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Best Local Similarity 99.2%;
Matches 121; Conservative (
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Homo sapiens
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AR124185.1
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1 (bases 1 to 4145)
Billiar, T.R., Nussler, A.K., Geller, D.A. and Simmons, R.L.

cDNA clone for human inducible nitric oxide synthase and process
for preparing same
Patent: US 5468630-A 1 21-NOV-1995;
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larity 99.2%; Pred. No. 1.2e-17;
Conservative 0; Mismatches 1;
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/wol_type="unassigned DNA"
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Sequence 1 from patent US 5468630.
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/note="16 A nucleotides"
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KAKGIILTCRSKXSCLGSIMTPKSLTRGPRDKRTPPDBELLPQAIEFYNQYYGSFKEAKIE
EHLARVEAUTKEIETTGTYQUTGDELIFATKQAMRAPRCIGRIQMSNLQVFDARSCS
TARENFEHICRHYWYSTNNGNIRSALTVFPQRSDGKHDFRWMAQLIRYAGYYOMPDGS
IRGDPANVETQLCIDLGWKPKYGRPDVVPLVLQANGRDFELFEIPPDLULEVAMEHP
KYSRFRRELEKWYALDAYANNILLEVGGLEFPGCFROWYMGTEIGVRDFCDVQRYNIL
EEVGRRMGLETHKLASLWADANVETNIAVYELBFROKQNYTIMDHISAAESFWKTWQNS
YRSRGGCPADMINLVPPMSGSIIPVFHQEMLNYVLSPFYYYQVEAWKTHVWQDEKRRP
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U31511.1 GI:951320
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 4062)
Park,C., Gianotti,C., Park,R. and Krishna,G.
Direct Submission
Submitted (11-JUL-1995) Chang-Shin Park, Lab. of Molecular
Immunology, NHLBI, 9000 Rockville Pike, Bethesda, MD 20892-1760, USA
                                                                                                                                                                                                                                                                    CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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1 (bases 1 to 4062)

Park, C.S., Park, R. and Krishna, G.

Constitutive expression and structural diversity of inducible isoform of nitric oxide synthase in human tissues

Life Sci. 59 (3), 219-225 (1996)
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                                                                                                                                                                   Length 4062;
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                                                                                                                                                                DB 6;
                                                                                                                                                              Score 120.4; DB 6;
Pred. No. 1.2e-17;
0; Mismatches 1;
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/produce=nitric oxide synthase"
/protein_id="AAB49041.1"
/db_xref="GI:951321"
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'gene="NOS"
'note="inducible isoform"
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                   /mol_type="genomic DNA'
                           1. .4062
/organism="unknown"
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cocation/Qualifiers
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/map="17cen-q11.2"
                                                                                                                                                              tch 46.7%;
al Similarity 99.2%;
121; Conservative
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Best Local S.
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HSU31511
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TITLE
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PAT 02-APR-1996

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Homo sapiens inducible nitric oxide synthase mRNA, complete cds.
L09210
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Sluto, M., Wang, S.C., Nakayama, D.K., Simmons, R.L., Snyder, S.H. and
Billiar, T.R.
Molecular cloning and expression of inducible nitric oxide synthase
PAT 07-0CT-1997
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                                                                                                               [Dasss 1 to 4145]
Billiar, T.R., Tzeng, E., Nussler, A.K., Geller, D.A. and Simmons, R.L.
Inducible nitric oxide synthase gene for treatment of disease
Patent: US 565855-A 19-AUG-1997;
Location/Qualifiers
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1 (bases 1 to 4145)
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                                                                                                                                                                                                                                                                 Length 4145;
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Proc. Natl. Acad. Sci. U.S.A. 90 (8), 3491-3495 (1993)
7682706
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linear
                                                                                                                                                                                                                                                                                             Indels
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/gene="inducible nitric oxide synthase"
/function="enzyme"
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/gene="inducible nitric oxide synthase"
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                                                                                                                                                                                                                                                              Score 120.4; DB 6;
Pred. No. 1.2e-17;
0; Mismatches 1;
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Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                    1. .4145
/organism="unknown"
/mol_type="unassigned DNA"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="hepatocyte"
161175
Sequence 1 from patent US 5658565.
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|...4145
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Best Local Similarity 99.2%;
Matches 121; Conservative 0
                                            GI:2479123
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|db_xref="GI:\2596176"
|trānslation="MACPWKFLFKTKFHQYAMNGEKDINNNVEKAPCATSSPVTQDDL
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QYHNLSKQQNESPQPLVETGKKSPESLVKLDATPLSSPRHVRIKNWGSGMTFQDTLHH
KAKGILTCRSKSCLGSIMTPKSLTRGPRDKPTPPDELLPQAIBFVNQYYGSFKEAKIB
                                                                                                                                                               EHLARVEAVTKEI ETTGTYQLTGDEL I FATKQAWRNAPRCIGR I QWSNLQVFDARSCS
TAREMPEH I CRHVRYSTNNGNI RSAI TVFPQRSDGKHDFRVWNAQLI RYAGYQMPDGS
I RGDPANVEFTQLCI DLGWKPKYGRFDVVPLVLQANGRDPELFEI PPDLVLEVAMEHP
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Moncada, S.E., Charles, I.G. and Palmer, R.M.

MONCAGE NITC OXIDE SYNTHASE AND GENE THEREFOR

INDUCIBLE NITRIC OXIDE SYNTHASE AND GENE THEREFOR

PATENT: WO 9423038-A 1 13-OCT-1994;

WELLCOME FOUND (GB)

Other publication AU 6287894 941024.

Location/Qualifiers

Location/Qualifiers

/mol type="unassigned DNA"
/db xref="taxon:9606"
/cell type="CHONDROCYTE"
/226. 3687
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46.7%; Score 120.4; DB 8; Length
Best Local Similarity 99.2%; Pred. No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels
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/gene="inducible nitric oxide synthase"
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PRI 13-JAN-1994

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/ procein_id="CAASISTS.1"

/ db_xref="G141453"
/ dr_xref="G141453"
/ db_xref="G141453"
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QNLQGYELSCHOOLDGYLAVQALFEPER
QTVELEALDESGSSWWSDKRLPPCTSCALGALTYFDTTLPQTLLQGALGAVATEBEPR
QTVELALLGCPSESGSWWSDKRLPPCTLEVLEEPSLNGAGFLLSQLPILKPRFYSISSSR
DHTPTEIHLTVAVVTYHTNDGQGPLHHGVCSTWLNSLKPQDPVPCFVRNASGFHLPED
PSPPCTLICPGCATAPRSPWQQRLHDSQHKQGSWTLYPCGDNPDBDITYOGEML
EMAQKGYLHAVHTAYSRLPGRSPKVAYDILAGQLASBVLRVLHKEPGHLYVCGDVRM
RDVAHTLKQLVAAKLKLNEEQVEDYFFQLKSQKRYHEDIFGAVFPYEAKKDRVAVQPS
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Submitted (23-APR-1993) I. Charles, Wellcome Research Laboratories,
Ble. 113, Deot. of Cekk Biology, Langley Park, Beckenham, Kent, BR3
3BS, UK
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Cloning, characterization, and expression of a cDNA encoding an inducible nitric oxide synthase from the human chondrocyte Proc. Natl. Acad. Sci. U.S.A. 90 (23), 11419-11423 (1993)
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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99.2%; Pred. No. 1.2e-17;
tive 0; Mismatches 1;
                                                                                                                                                                                                              4164 bp mRNA
H.sapiens mRNA for nitric oxide synthase.
X73029
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/product="nitric oxide synthase"
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/gene="INOS"
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'organism="Homo sapiens"
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Homo sapiens (human)
Homo sapiens
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Best Local Similarity 99.2'
Matches 121; Conservative
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KRSRGGCPADMIMUVPPMSGSITPVFHQEMLAYVLSPPYYVQVBAWKTHVWQDEKRRP
KRREIPLKVLVKAVLFACLIMRKTMASRNAFRYTILFATETGKSEALAWDLGALFSCAFN
PKVVCMYRLSCLEERELLIVYTSTFGNGDCPGNGSKLKKGLFMLKZLINNKFRYAVF
GLGSSMYPRFCAFAHDIDQKLSHLGASQLTPWGEGDELSGQBDAFRSWAVQTFKRAAC
PTD VRGKQHTQIPKLYSTWYWDPHTKLQVGOSPDLDISKALSSMHAKVYFTRRLKSR
QNLQSPTSSRATILVELSCEGGGGLAYLLEGSGULDGKALSMHAKVFTRRLKSR
QTVRLEALDESGSYWVSDKRLPPCSLSQALTYFLDITTPPTQLLLQKLAQVATEEFER
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DHTPTEIHLTVAVVTYHTRDGGGPLHHGVCSTWLNSLKPQDPVPCFVRNASGFHLPED
PREPCTLIGPOTGIAPPRSFWOORLHPSQHKGYRGGRWTLVFCGRRPEDHIYQBEML
EMAGKGVLHAVHTAYSRLPGKPKVYVQDILRQQLASEVLRVLHKEPGHLYVCGDVRMA
RDVAHTKQLVAAKLKLNEEQVEDYFFQLKSQKRYHEDIFGAVFPXEKKDRVAVQPS
SLEMSAL"
                              KAKGILTCRSKSCLGSIMTPKSLTRGPRDKPTPPDELLPQAIEFVNQYYGSFKEAKIE
EHLARVEAVTKEIETTGTYQLTGDELIFATKQAWRNAPRCIGRIQWSNLQVFDARSCS
                                                                                           TAREMFEHICRHVRYSTNNGNIRSAITVFPQRSDGKHDFRVWNAQLIRYÄGYQMDDGS
IRGDPANVEFTQLCIDLGWKPKYGRFDVVPLVLQANGRDFELFEIPPDLVLEVAMEHP
KYEWFRELELKWYALPAVANMLLEVGGLEFPGCPFNGWYMGTEIGVRDFCDVQRYNIL
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Cocks B.G., Stuart, S.G. and Seilhamer, J.J.
Compositions for the detection of blood cell and immunological response gene expression
Patent: US 6607879-A 1407 19-AUG-2003;
Incyte Corporation; Palo Alto, CA
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Pred. No. 1.2e-17;
0; Mismatches 1
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Sequence 1407 from patent US 6607879.
AR380862
AR380862.1 GI:40088496
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99.2%;
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Matches 121; Conserv
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EMAQKGVLHAVHTAYSRLPGKPKVYVQDILRQQLASEVLRVLHKEPGHLYVCGDVRMA
RDVAHTLKQLVAAKLKLNEEQVEDYFFQLKSQKRYHEDIFGAVFPYEAKKDRVAVQPS
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QTRLEBLDESGSYWYGDKRLPPCSLEQALIYSPDITTPPTQLLLQKALAQVATEBERG
QTLEALCQPSEYSKKTNSPTFLEVLEEPPSLRVSAGFLLSQLPILKERFYSISSSR
DHTPTEIHLTVAVVTYHTGDGQGPLHHGVCSTMLNSLKPQDPVPCFVRNASAFHLPED
                                                                                                                                          1. .35764

/organism="Adenoviral expression vector Ad-hiNOS"

/organism="Adenomic DNA"

/db xref="taxon:170704"

/note="recombinant human adenovirus type:5 encoding human

iNOS; derived from pAdLox shuttle vector and donor
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                                               Direct Submission
Submitted (18-JUL-2001) Surgery, University of Pittsburgh, 300
Technology Drive, Pittsburgh, PA 15219, USA
Location/Qualifiers
Shapiro, R., Gao, W., Tzeng, E., Robbins, P.D., Timoty, B.R. and
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46.7%; Score 120.4; DB 11; Length 35764;
Best Local Similarity 99.2%; Pred. No. 8.4e-18;
Matches 121; Conservative 0; Mismatches 1; Indels 0; (
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/note="SV40 early polyadenylation signal"
4961. .4965.
/note="SV40 polyadenylation signal"
5044. .5077
/bound_molety="Loxp"
35661. .35764
/note="terminal repeat"
/rpt_type=inverted
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produce=inducible nitric oxide synthase"
protein_id="AALO2120.1"
/db_xref="GI:15636800"
                                                                                                                                                                                                                                                                                                              1. .103
/rote="terminal repeat"
/rpt_type=inverted
193. .354
/note="packaging site"
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/gene="iNOS"
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/gene="iNOS"
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Adenoviral expression vector Ad-hiNOS, complete sequence.
AY046510
                             970 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1029
                                                                                                                            PAT 03-FEB-2004
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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(Dases 1 to 35764)
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       CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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Adenoviral expression vector Ad-hiNOS
Orber sequences; artificial sequences; vectors.
1 (bases 1 to 35764)
Shapiro,R., Gao,W., Tzeng,E., Robbins,P.D., Timoty,B.R. and
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Pred. No. 1.1e-17;
0; Mismatches 1;
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PE Corporation (NY) (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      Sequence 9599 from Patent W002068579.
CQ723665
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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1 (bases 1 to 4150)

Luss,H., Li,R.-K., Shapiro,R.A., Tzeng,E., McGowan,F.X., Yoneyama,T., Hatakayama,K., Geller,D.A., Mickle,D.A.G., Simmons,R.L. and Billiar,T.R.

Dedifferentiated human ventricular cardiac myocytes express inducible nitric oxide synthase mRNA but not protein in response to IL-1, TNF, IFNgamma, and LPS

J. Mol. Cell. Cardiol. 29 (4), 1153-1165 (1997)
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                                                                    PAT 24-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF068236 4150 bp mRNA linear PRI 07-JUN-195
Homo sapiens inducible nitric oxide synthase (NOS) mRNA, complete
                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                        Keller,E.T., Gravenstein,S. and Hall,D.M.
Treatment of Viral infiluenza with antisense oligonucleotides
Patent: WO 0078846.A 3 28-DEC-2000;
Eastern Virginia Medical School (US)
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Submitted (26-MAY-1998) Pharmacology, Westf.Wilhelms-Univ.,
Domagkstr. 12, Munster D-48149, Germany
Location/Qualifiers
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Luss, Li, Li,R.-K., Shapiro,R.A., Tzeng,E., McGowan,F.X.,
Yoneyama, T., Hatakayama, K., Geller,D.A., Mickle,D.A.G.,
Simmons,R.L. and Billiar,T.R.
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Pred. No. 2.7e-17;
0; Mismatches 2;
                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                               /mol_type="unassigned DNA" /db_xref="taxon:9606"
                                                             Sequence 3 from Patent WO0078946.
AX067222
                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                     AX067222.1 GI:12544879
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AF068236
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                                RESULT 28
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/protein_id="AAC19133.1"
/db_xref="G1:3192917"
/tanslation="MACPWFLFKTKFHQYAMNGEKDINNNVEKAPCATSSPVTQDDL
QYHNISKQQNESPQPLVETGKKSPESIJVKLDATPLSSPRHVNIKNWGSGMTFQPTLHH
KAKGILTCRSKSCLGSIMTPKSLTRGPRDKPTPPDELLPQAIEFVNQYYGSFKEAKIE
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RDVAHTLKQLVAAKLKLNEEQVEDY FFQLKSQKRYHEDI FGAVFPYEAKKDRVAVQPS
SLEMSAL"
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Bos taurus clone CH240-54J11, WORKING DRAFT SEQUENCE, 16 unordered
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Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, H., Alsen, H., Alseroks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
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46.0%; Score 118.8; DB 8; Length 4150;
Best Local Similarity 98.4%; Pred. No. 2.7e-17;
Matches 120; Conservative 0; Mismatches 2; Indels 0;
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ACIS8064.2 GI:68266847
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
BOB taurus (cow)
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/db_xref="taxon:9606"
/call_type="cardiac myocytes"
1. 4I50
/gene="NOS"
235. 3696
/gene="NOS"
/note="NOS II"
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1 (bases 1 to 179504)
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Consensus quality: 174250 bases at least Q40
Consensus quality: 175616 bases at least Q30
Consensus quality: 17527 bases at least Q30
Estimated insert size: 174799; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu

Center code: BCM

Center project name: FDEA Center clone name: CH240-54J11 ----- Summary Statistics Assembly program: Atlas 3.0;

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Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Y., Chen, Z.,
Chacko, J., Chavez, D., Chen, G., Chen, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Chen, S., Chen, Y., Chen, Y., Chen, Z.,
Davis, C., Davis, C., Ding, Y., Dinl, H., Dinya, K.,
Dapar, R., Day, Carroll, L., Danda, C., Dederich, D.,
Dayla, M., Bosonto, M., Bugene, C., Bugar, R., Dinl, H., Dinya, K.,
Benotto, M., Bugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Bavee, K.,
Ban, A., Escotto, M., Bugene, C., Paran, C.A., Garrer, M., Garza, M.,
Franser, C. M., Gabisi, A., Ganta, R., Gardi, R., Garzi, M., Guerra, M., Mandun, P., Mandun, P., Mandun, P., Mantin, Y., London, P., Londoch, P., Martin, K., Martin, R., Manula, M., Ma
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On Jun 28, 2005 this sequence version replaced gi:60498836.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
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Direct Submission
Direct (04-MAR-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cow Genome Sequencing Consortium.
Direct Submission
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JOURNAL
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Center: Baylor College of Medicine

COMMENT

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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 16 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                              2: contig of 1552 bp in length
4: gap of 50 bp
5: contig of 10182 bp in length
5: contig of 46345 bp in length
4: gap of 395 bp
5: contig of 46381 bp in length
5: gap of 50 bp
6: contig of 8663 bp in length
6: gap of 50 bp
7: contig of 5127 bp in length
7: gap of 50 bp
7: contig of 51200 bp in length
7: gap of 50 bp
7: contig of 15200 bp in length
7: contig of 15200 bp in length
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7: contig of 15200 bp in length
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7: contig of 15200 bp in length
7: gap of 50 bp
7: contig of 15200 bp in length
7: gap of 50 bp
7: contig of 15200 bp in length
7: gap of 60 bp
7: contig of 15200 bp in length
7: gap of 150 bp
7: contig of 15200 bp in length
7: gap of 150 bp
7: contig of 15200 bp in length
7: gap of 150 bp
7: contig of 1
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contrig of 1040 bp in length
contrig of 1060 bp in length
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/db_xref="taxon:9913"
/clone="CH240-54J11"
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/organism="Bos taurus"
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102956. .103005
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111669. .111718
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120507. 120556
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11785. .11834
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58180. .58574
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STROGCPADMYTLYPPEISGSTPVFHOEMLNYTLEPPYYQVORAMKTHWODERRRPOR
REITRFKVLIKAVFFASITPVFHOEMLNYTLEPPYYYOVAMKTHWODERRRPOR
REITRFKVLIKAVFFASITERSPRENGABORGEKKKSLLMLKELTINKFRYAVFGL
GSSMYPOFCAFAHDIOCKLSQLGASQLAPTGEDEBELSGGEBAFRSMAVOTFKACCETF
DVSGKHHIEIPKLYTSSVTWDPHYTRLVQDSEPLDINKALSSMHAKPVFTMRLKSQON
LQSPKSSRTTLLVALSGGSQAPSYLDGEHLGVFPCNQPALVGGILLERVVDGFPAPHQ
MRLETLCQPSDYNWKFTNSPTELSVEEPPSLLKSVFCNQPALVGGILLERVVDGFPAPHQ
TETLCQPSDYNWKFTNSPTELSVEEPPSLLKSVFSTLLSQLPILKRAVJATTSSSRDL
TPTTHILTVAVLTYTSTRDGGGPLHHGVCSTWLSSLKPQDDPVCFVRSASGFQLAFBERRR
RPCILIGPGTGIAPFRSFWQORLHEABHKGLGGGRMTLVFGCRRFBEBDHLYWBEBMLEW
                                                                                                                                                                                                                                                                                                           ARKGVLHEVHTAYSRLPDQPKVYVQDILRQRLAGEVLRVLHEEQGHLYVCGDVRMARD
VAHSLKQLMATALSLNEEQVEDYFPQLKNQK"
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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S229P690FE2.T0 GermanShepherd Cania familiaris STS genomic,
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Fax: 6172580903
Email: kerali@genome.wi.mit.edu
Emier A: No sequence submitted
Primer B: No sequence submitted
                                                                                                                                                                                                                                                                                                                                                                                                        39.8%; Score 102.8; DB 4 ilarity 90.2%; Pred. No. 1.4e-13; Conservative 0; Mismatches 12
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Matches 110; Conserv
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KEYWORDS
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Ovis aries inducible nitric oxide synthase mRNA, partial cds.
AF223942
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QEMFEHICRHVRYATNNGNIRSAITVFPQRSDGKHDFRVWNAQLIRYAGYQMPDGSIR
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
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Mershon, J.L. and Clark, K.E.

Mershon, J.L. and Clark, K.E.

Direct Submission

Submitted (12-5702000) Department of Obstetrics and Gynecology,
University of Cincinnati Medical Center, 231 Bethesda Ave,
Cincinnati, OH 45267-0526, USA

Location/Qualifiers
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Mershon, J. L., Baker, R.S. and Clark, K.E.
Estrogen increases iNOS expression in the ovine coronary artery
Am. J. Physiol. Heart Circ. Physiol. 283 (3), H1169-H1180 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 45.0%; Score 116; DB 14; Length 179504; Similarity 89.3%; Pred. No. 6.7e-17; 25; Conservative 0; Mismatches 15; Indels 0;
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173901. .174000
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175180. .175279
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    . 2838
    /organism="Ovis aries"
    /mol_type="mRNA"
    /db_xref="taxon:9940"

125884. .125933
/estimated length=50
129690. .129739
/estimated length=50
144940. .145284
                                                                                                                /estimated length=345
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Best Local S
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AUTHORS
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AUTHORS
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LOCUS
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Submitted (03-OCT-2001) Cellular and Molecular Pharmacology,
Servier Research Institute, 125, Chemin de Ronde, Croissy sur Seine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="DarscstagemfehicrhlryatnngnirsaltvPpqrsDgkdd
RywnagoliraryagydppottidDparvbrPqlciDbawkryagrbVvbLvLhabGR
DPBLFRIPPDLVLEVPWEHPRYEWPGBLBLKWYALPAVANMLLEVGGLBFPGGFPNGW
YMGTBIGVRDFCDVQRYNILEEVGRRMGLETHKLASLWKDRAVVEINVAVLHSFQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROD 29-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 GGCTACCAGATGCCTGATGGCACCATCATAGGGGACCCGGCCAGCGTGGAGTTCACCCAG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GGCTACCAGATGCCAGATGGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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/chromosome="11"
join(1. 25,1252. 1407,7604. .7673,8781. .8900,10610. ..
14382. .14544,15433. .15524,16591. .16732,16830. .16969,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF427516 38817 bp DNA linear ROD 29-OCT-20
Mus musculus inducible nitric oxide synthase gene, complete cds.
AF427516
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Genomic structure of the murine inducible nitric oxide synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                  PathoBiol., Univ. of Minn., 1971
MN 55108, USA
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                 Murtaugh, M.P., Pampusch, M.S., Harsch, S. and Bennaars, A.M. Direct Submission
Submitted (27-MAY-1996) Vet. PathoBiol., Univ. of Minn., Commonwealth Ave., St. Paul, MN 55108, USA
Location/Qualifiers
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                         /cell_type="ConA, LPS stimulated splenocytes"
<1. .>647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 647;
                                                                                                                                                                                                                                                                                                                                                                                                                              'product="inducible nitric oxide synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.6%; Score 99.6; DB 4;
88.5%; Pred. No. 9.4e-13;
iive 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAB40614.1"
/db_xref="GI:1777980"
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/mol type="genomic DNA"
/strain="CD-1"
                                                                                                                                                                                                                         /organism="Sus scrofa"
/mol type="mRNA"
/db xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .38817
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Mus musculus
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Unpublished
2 (bases 1 to 38817)
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(bases 1 to 647)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection was carried out by SSAHA-SNP. 1637780 SNPs were annotated with alleles from the boxer and the poodle. The validation rate for these SNPs was estimated at approximately TBD%. Internal-WGA-discovery (I-WGA): A third set of SNPs were discovered by comparing reads in the WGA assembly. SNPs were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSUS SCIPPED THE STATE OF SUBSCIPPED THE STATE OF SUBSCIPPED TO SUBSCIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             defined as mismatch positions that had a base quality of >= 30 on both reads in a region that aligned without gaps, and with at most one additional mismatch in the ten flanking at least one additional read had to confirm it. 731476 SNPs were annotated with alleles between the two boxer alleles. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (pig)
Sus scrofa
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                          A second set of SNPs was generated using a similar methodology except that the contigs from the 1.5x poodle assembly (Kirkness 2003) were used instead of WGS reads. Since this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351
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reads were placed uniquely on the CanFam1.0 boxer assembly
                                                                                                485941 SNPs were
annotated with alleles from the boxer and the breed or canid from
which the particular
                                         and SNP detection was carried out by SSAHA-SNP. 863872 reads were annotated as STSs and
                                                                                                                                                                                                                                                                                                                                                                                           sequence lacked base quality scores, arbitrary quality scores of phred 40 were assigned before the poddle sequence was placed uniquely on the CanFaml.0 becar assembly and SNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                          read came. The validation rate for these SNPs was estimated at approximately 98%.
WGA-discovery (WGA) of Boxer/Poodle SNPs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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/strain="GermanShepherd"
/db_xref="taxon:9615"
/map="+ 9 22-578 34794085-34794641"
/clone lib="GermanShepherd"
/loop lib="GermanShepherd"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Canis familiaris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was estimated at approximately TBD%.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTACCCGGCCCAGCCTCAGCCRCCGGC 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               validation rate for these SNPs
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Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350
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ACCESSION
VERSION
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SSU59390
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SOURCE
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regions were either double-tranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) = 30); an attempt was made to resolve all sequencing problems, such as compressions and respeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. Sequence from the Mouse Genome Sequencing Consortium whole genome shocgun may have been used to confirm this sequence. Sequence data from the whole genome shocgun alone has only been used where it has a phred quality of at least 30. RP23-34132 is from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="RPCI-23"
join(3524. 35276,44658. 44798,46730. .46822,47763.
/locus_tag="RP23-341122.1-001"
join(35224. .35276,44658. .44798,46730. .46822,47763.
_locus_tag="RP23-341J22.1-001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /jours tag="RP23-341022.2-001"
join(129427. 129635,130862. .131017,137214. .137
138391. 138510,140220. 140368,143992. .144154,
14643. 1445134,146201. 146342,146440. 146579,
148619. 148793,148888. 148989,153300. 153494,
153872. 153954,154779. 154423,154609. 154613,
156487. 155536,156853. 157077,157723. 1579898,
161443. 161650,163535. 163622,163980. 164101,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="match: ESTB: Em:BY102364.1"
                                                                                                                                                                                                                                                                                                                                                                      Center: Wellcome Trust Sanger Institute
Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus_tag="RP23-341J22.1-001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="RP23-341J22.1-001"
129427. .168894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
|mol_type="genomic DNA"
|db_xref="taxon:10090"
|chromosome="11"
|clone="RP23-341J22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="Nos2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .178443
                                                                                                                                                                                                                                                                                                                                                      Genome Center
   Hopkins, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polyA_signal
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                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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AUTHORS
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                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / CEARS LAIL SOLVER TO SERVING THE CONTROL OF THE C
                16673 GGCTACCAGATGCCCGATGGCACCATCAGAGGGGATGCTGCCACCTTGGAGTTCACCCAG 16732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16613 CAGCGGAGTGACGGCAAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGGTACGCT 16672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL592185
Mouse DNA sequence from clone RP23-34JJ22 on chromosome 11 Contains a novel gene, the Nos2 gene for inducible macrophage nitric oxide synthase 2 and the 3' end of the Lgals9 gene for soluble galactose binding lectin 9, complete sequence.

AL592185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLDESGSYWWKDKRLPPCSLSQALTYFLDITTPPTQLQLHKLARFATDETDRQRLEAL
CQPSSYNDWKRSNNPTFLEVLEEPSGLHVPAAFLLSQLPILKRRYYSISSQOHTPSE
VHLTVAVVTYRTRDGQPLHGVCSTRIRNLKPQDPVPCFVRSVSGFQLPEDPSQPCI
LIGFOTGIAPPRSFWQQRLHDSQHKGLKGGRNSLVFGCRHPEEDHLYQEEMQEWVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLFQVHTGYSRLPGKPKVYVQDILQKQLANEVLSVLHGEQGHLYICGDVRMARDVATT
LKKLVATKLNLSEEQVEDYFFQLKSQKRYHEDIFGAVFSYGAKKGSALEEPKATRL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 178443)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.3%; Score 98.8; DB 9; Length 38817; llarity 78.7%; Pred. No. 7.6e-13; Conservative 1; Mismatches 33; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16733 GTA-CTGACTCAGCCTCTCCTAGATCCCTGTGGGGGGGACCC 16775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTACCCGGCCCAGCCTCAGCCRCCGGCCATTGGGGCGGGGAGCC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL592185.35 GI:21213991
HTG; lectin; Lgals9; Nos2.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 129; Conserv
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DEFINITION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL592185
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.46822,47763. .52534)

CDS

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146223 CAGCGGAGTGACGGCAAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGGTACGCT 146282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC036147

Mus musculus chromosome 11 clone RP23-240G13 map 11, WORKING DRAFT SEQUENCE, 10 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /locus tag="RP23-12113.3-001"
join/AL592551.10:198630. 198683,
AL592551.10:206760. 206849, AL592551.10:210272. 210473,
AL592551.10:212034. 212144, complement (176354. 178443),
complement (176538. 176673), complement (176084. 176134),
complement (175517. 175558), complement (174638. 174726),
/gene="Lga189". 174194), complement (174035. 172181)
                                                                                                 //ocus tag="RP23-12113.3-001"
join(AL592551.10:198515. .198683,
AL592551.10:206760. .206848, AL592551.10:210272. .210473,
AL592551.10:212034. .21144, complement (176638. .176673),
complement (17688. .176134), complement (175558. .175558),
complement (174638. .174726), complement (174332. .174494),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus tag="RP23-12113.3-002"
join(AL592551.10:198630. 198683,
AL592551.10:206760. 206848, AL592551.10:210272. 210473,
AL592551.10:212034. 212144, complement (178354. 178443),
complement (176538. 176673), complement (176684. 176134),
complement (175517. 175558), complement (174638. 174726),
complement (174332. 174494), complement (172035. 172181))
complement(174638. .174726),complement(174332. .174494),
                                                                                                                                                                                                                                                                                                                                                                                                         /jocus tag="RP23-12113.3-001"
/product="lectin, galactose binding, soluble 9"
/note="match: BSTs: Em.AI042899.1 Em:AI04329.1
Em.AI530150.1 Em:AM541736.2 Em:BI647345.1 Em:BI647383.1
Em:BR657219.1 Em:BM244207.2
match: cDNAs: Em:BC003754.1 Em:U55060.1"
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/product="lectin, galactose binding, soluble 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9; Length 178443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTA-CTGACTCAGCCTCTAGATCCCTGTGGGCAGGGACCC 146385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTACCCGGCCCAGCCTCAGCCRCCGGCCATTGGGGCGGGGAGCC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 98.8; DB 9;
Pred. No. 6.1e-13;
1; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /locus tag="RP23-12113.3-001"
complement (171642. .171647)
/gene="Lgals9"
                                      complement (171614. .172181))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC036147.4 GI:28570424
HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (171618)
/gene="Lgals9"
                                                                                                                                                                                                                                                                                                                                                                                  /gene="Lgals9"
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Best Local Similarity 78.7
Matches 129; Conservative
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                 /product = "match: Caride gynthase 2, inducible, macrophage" /note="match: ESTs: Em:AA512708.1 Em:BE372884.1 Em:EG974881.1 Em:EG974881.1 Em:EG974881.1 Em:EW747653.1 Em:EW77650.1 Em:AF06592.2 Em:AF06592.2 Em:AF06592.2 Em:AF06592.1 Em:AF06592.2 Em:AF06592.3 Em:AF06592.1 Em:AF06592.2 Em:AF06592.3 Em:AF06592.1 Em:M92649.1 Em:U43428.1 Em:D12520.1 Em:M94373.1 Em:U43428.1 Em:D177137283.1 Em:D12520.1 Em:M94373.1 Em:M9498.1 Em:AF04923.1 Em:BF799.1 Em:M9498.1 Em:M9498.1 Em:AF0433.1 Em:BF799.1 Em:AF0433.1 Em:BF799.1 Em:BF7999.1 Em:BF799.1 Em:BF799.1 Em:BF799.1 Em:BF799.1 Em:BF799.1 Em:BF799.1 Em:BF799.1 Em:BF799.1 E
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QHICHHILYATNNGNIRSAITVPPQRSDGKHDFRLANSQLIRYAGYQWPDGTIRGDAA
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KSSRTTLLVQLTFEGGSRGPSYLPGEHLGIFPONQTLLERYVDCGTLERYVDCGTUERVOCTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | db xref="InterPro:IPR001094"
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| TCKSKGCLGSIMNPKSLIRGPRDKPTPLEELLPHAIEFINQYYGSFKEAKIEEHLARL
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LKKLVATKLNLSEEQVEDYFFQLKSQKRYHEDIFGAVFSYGAKKGSALEEPKATRL"
168842. .168847
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CQPSEYNDWKFSNNPTFLEVLEEFPSLHVPAAFLLSQLPILKPRYYSISSSQDHTPSB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="nitric oxide synthase 2, inducible, macrophage"
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/db_xref="GI:56206296"
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join(AL592551.10:198515. .198683,
AL592551.10:206760. .20648, AL592551.10:210272. .210473,
AL522551.10:212034. .212144, complement (176638. .176673),
complement (176084. .176134), complement (175517. .175558),
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/standard_name="OTTYMUSBO000000202"
/note="match: proteins: Sw.:019114 Sw.:29477 Tr:AAH62378
Tr:AAL24076 Tr:097604 Tr:Q8R410 Tr:Q9BDH6 Tr:Q9N175"
       .166244,168294. .168894)
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/locus_tag="RP23-341J22.2-001"
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|locus_tag="RP23-341J22.2-001"
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168885
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       .165284,166050.
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Quality coverage: 12.2 in Q20 bases; agarose-fp Quality coverage: 12.0 in Q20.

Quality coverage: 12.0 in Q20.

NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8418 68517; gap of 100 bp

8518 141054; contig of 72537 bp in length

1055 141154; gap of 100 bp

7739 16738; contig of 26584 bp in length

7739 16738; gap of 100 bp

7739 203042; contig of 35204 bp in length

1043 203142; gap of 100 bp

113 236456; contig of 33314 bp in length.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of 100 bp
contig of 13750 bp in length
gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of 100 bp
contig of 12807 bp in length
gap of 100 bp
                                                                                                                                                                                                                                                                                                                   contig of 33985 bp in length
gap of 100 bp
contig of 1045 bp in length
gap of 100 bp
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contig of 2936 bp in length
gap of 100 bp
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contig of 3394 bp in length
gap of 100 bp
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167739. .167838
/estimated_length=100
167839. .203042
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/estimated_length=100
34086. .35130
/note="assembly_fragment"
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41761. .55510
/note="assembly_fragment"
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55611. .68417
/note="assembly_fragment"
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68518. .141054
/note="assembly_fragment"
141055. .141154
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/note="assembly_fragment
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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35231. .38166
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2 (bases I to 236456)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DaArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, F., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grahm, L., Karatas, A., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Landaraes, R., Landers, T., Maratus, N., McBwan, P., McGurk, A., McKernan, K., McGretter, R., Marquis, N., McBwan, P., McGurk, A., McKernan, K., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Nihova, T., Miranda, C., Mlenga, V., Morrow, J., Whypy, T., Naylor, J., Nihova, T., Miranda, C., Mlenga, V., Morrow, J., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stancos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Valen, Y., Viel, R., Wo, A., Milson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Direck, Subrate, M., Cannon, J., Sanous, A., Milson, B., Wu, X., Wyman, D., Ye, W. J., Shriens, M., Milson, B., Wu, X., Wyman, D., Ye, W. J., Shriens, M., Milson, B., Wu, X., Wyman, D., Ye, W. J., Shriens, M., Milson, B., Wu, X., Wyman, D., Ye, W. J., Shriens, M., Milson, B., Wu, X., Wyman, D., Ye, W. J., Shriens, M., Milson, B., Wu, X., Wyman, D., Ye, W. J., Shriens, M., Milson, B., Wu, X., Wyman, D., Ye, W. J., Shriens, M., Milson, B., Wu, X., Wyman, D., Ye, W. J., Shriens, M., Milson, B., Wu, X., Wyman, D., Ye, W. J., Shriens, M., Milson, B., Wu, X., Wyman, D., Ye, W. J., Shriens, M., Wilson, B., What, M., What, M., Shriens, M., Wilson, B., What, M., Wha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; M77815; 40% of reads Sequencing vector: Plasmid; n/4»; 60% of reads Sequencing vector: Plasmid; n/4»; 60% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 233217 bases at least Q40 Consensus quality: 24384 bases at least Q20 consensus quality: 215022 bases at least Q20
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Insert size: 235556; sum-of-contigs
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Muzny, D.Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,

Anyalebechi, V., Aoyagi, A., Aydedi, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnatead, M., Benahmed, F.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnatead, M., Benahmed, F.,

Baldwin, D., Bandy, C., Burch, P., Burchl, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,

Cardenas, V., Carter, K., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Davila, M.L., Davis, C., Dary, Carroll, L., De Anda, C., Dederich, D.,

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Divya, K.,

Egan, A., Escotto, M., Eugene, C., Brans, C.A., Falls, T., Fan, G.,

Frandac, S., Finley, M., Flaggy, N., Forbes, L., Foster, M., Guerza, M.,

Gebregocygis, B., Geer, K., Gill, R., Gardy, M., Guerra, W., Guevara, W.,

Gebregocygis, E., Hallad, W., Handl, C., Hamilton, K.,

Harvey, Y., Havlak, P., Hawes, A., Hladerson, N., Herandez, J.,

Harvey, Y., Havlak, P., Hawes, A., Hladerson, N., Herandez, J.,

Jackson, L., Jacob, L., Jang, H., Johnson, B., Johnson, R., Johnson, R., Johnson, L., Jacob, L., Jang, H., London, P., Longace, S., Lopez, J.,

Liu, J., Liu, M., Liu, Y., Loho, H., Lewis, L., Li, Z., Liu, J.,

Karpathy, S., Kelly, S., Khaly, S., Khan, Z., King, L., Kovar, C.,

Karpathy, S., Mcle, M., Martin, R., Martin, R., Martin, R., Martin, R., Mandyun, B., Mandyun, B., Mandyun, B., Mantiney, S., Mcle, M., Martin, R., Martin, R., Mandyun, M., Mantiney, S., Mcle, C., Mangum, A., Mangum, M., Morris, S., Munidasa, M., Norris, S., Parks, K.,

Platernah, W., Mainer, G., Minja, E., Wontemayor, J., Way, P., Partankoch, C., Nangum, R., Mandol, M., Olarno, P., Pall, H., Perez, L., Perez, L., Plankock, Pally, R., Perez, L., Perez, L., Plankock, R., Perez, M., Perez, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS AĞ105495 430182 bp DNA linear HTG 11-OCT-2002
DEFINITION Rattus norvegicus clone CH230-216J16, WORKING DRAFT SEQUENCE, 11
                                                                                                                                              61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                98 GGCTACCAGATGCCCGATGGCACCATCAGAGGGATCCTGCCACCTTGGAGTTCACCCAG 157
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16; Indels
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HTG; HTGS_PHASEI; HTGS_DRAFT; HTGS_FULLTOP.
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     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNO230468 163 bp DNA linear ROD 29-JUN-1999
Rattus norvegicus gene encoding inducible nitric oxide synthase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keinanen, R., Vartiainen, N. and Koistinaho, J.
Molecular cloning and characterization of the rat inducible nitric
synthase (iNOS) gene
Gene 234 (2), 297-305 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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inducible nitric oxide synthase; iNOS gene.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Rattus norvegicus
Rattus norvegicus
Mamalia; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
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Submitted (26-JUN-1998) Keinanen R.A., A.I. Virtanen Institute,
University of Kuopio, P.O. Box 1627, FIN-70211 Kuopio, Finland
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                               Query Match 38.3%; Score 98.8; DB 14; Length 236456; Best Local Similarity 78.7%; Pred. No. 5.8e-13; Aatches 129; Conservative 1; Mismatches 33; Indels 1; C
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/gene="iNOS"
/product="inducible nitric oxide synthase"
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/strain="Wistar Kyoto"
/db_xref="taxon:10116"
/clone_lib="cosmid (SuperCos1) library"
<1. .15
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/usedin=AJ230462:INOS_CDS
       /note="assembly_fragment"
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203143. 236456
/note="assembly_fragment
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1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
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Best Local Similarity 87.1%; Pred. No. 8.1e-13;
Matches 108; Conservative 0; Mismatches 16; Indels
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4220...
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/ Note = "clone_boundary
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Siseon, T., Sitter, C.D., Smajs, D., Sned, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Valas, R., Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Warten, R., Wei, K., Whilson, R., Wilson, R., Wilson, R., Wilson, R., Wilson, R., Wilson, R., Waldri, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Wainstock, G. and Gibbs, R.A.
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

Contact: hgsc-help@bcm.tmc.edu

Center project Information
Center clone name: CH30-216316

Center project name: CH30-216316

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Submitted (09-TAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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NOTE: This sequence may represent more than one clone.
NOTE: This is a "working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Rat Genome Sequencing Consortium.
Direct Submission
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2 (bases 1 to 430182)
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Direct Submission

Direct Submission

Submitted (13-M94-2003) Human Genome Sequencing Center, Department Submitted (13-M94-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:23123790. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bom.tmc.edu/projects/raf/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                     Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 240200)
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Consensus quality: 232006 bases at least Q40
Consensus quality: 234013 bases at least Q30
Consensus quality: 235789 bases at least Q20
Estimated insert size: 243219; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
Direct Submission
Unpublished
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Contact: hgsc-help@bcm.tmc.edu
------- Project Information
Center project name: GIZT
Center clone name: GH230-22205
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Center code: BCM
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/db xref="taxon:10116"
/clone="CH230-22205"
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/estimated length=unknown
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      33717 GGCTACCACATGCCCCAATGGCACCATCAGAGGGGATCCTGCCACCTTGGAGTTCACCCAG 33776
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Rattus norvegicus clone CH230-222O5, WORKING DRAFT SEQUENCE, 2
unordered pieces.
                                                                                                    61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 120
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone.
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Sturognaturi, mirotoae; murinae; katcus.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86288 GGCTACCAGATGCCCGATGGCACCATCAGAGGGGATCCTGCCACCTTGGAGTTCACCCAG 86229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314746 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus clone CH230-126J7, *** SEQUENCING IN PROGRESS
***, 23 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.1%; Score 98.4; DB 14; Length 240200; 87.1%; Pred. No. 7.1e-13; ive 0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC106421.5 GI:30581088
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Rattus norvegicus (Norway rat)
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Best Local Similarity
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Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:24819147.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.twc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Liu, W., London, P., Longacre, S., Lopez, J., Lorenshhwa, L., Loulseade, H., Lozado, R.J., Lu, X., Ma, J., Mahlewa, L., Loulseade, H., Lozado, R.J., Malloy, K., Mangum, A., Mahnend, M., Malloy, K., Mangum, A., Manduari, M., Martin, K., Martin, R., Martinez, E., Mached, M.P., McMedil, T.Z., Menene, E., Milosavljevic, A., Miner, G., Minia, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nanceled, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nanceled, M., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, M., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pully, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Riiz, S. J., Sanders, W., Savery, G., Scherer, S., Socht, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, R., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Wang, S., Warten, J., Walker, M., Trongs, S., Warten, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, U., Yu, F., Zhou, J., Zhou, J., Yoon, L., Yoon, L., You, Williams, G., Wallson, R., Walse, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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Direct Submission

Direct Submission

Direct Submission

Direct Submission

Norley, K. C.

Direct Submission

Norley, K. C.

Direct Submission

Norley, K. C.

Norley, K. C.

Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (Bases I to 314746)

Direct Submission
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Consensus quality: 291712 bases at least Q30
Consensus quality: 295672 bases at least Q30
Estimated insert aize: 299042; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: BCM
Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Out the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299753: gap of unknown length
754 209753: gap of unknown length
754 301958: contig of 2205 bp in length
759 304773: contig of 2115 bp in length
774 3084773: gap of unknown length
778 308477: contig of 3904 bp in length
778 308277: gap of unknown length
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894 311993: gap of unknown length
778 31278: gap of unknown length
778 314746: contig of 2753 bp in length
778 200416161878
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contig of 1574 b
gap of unknown l
contig of 1805 b
gap of unknown l
contig of 1121 b
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contig of 1755
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                                                                                                                                                                                                                                                                                                                                                      Query Match
38.1%; Score 98.4; DB 14; Length 314746;
Best Local Similarity 87.1%; Pred. No. 6.9e-13;
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                    OM nucleic - nucleic search, using sw model
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258
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Adz75764 Human ind	Aah78096 Nucleotid	Aah78095 Nucleotid	Adv42931 Human psy	Abx76286 Lung canc	Ada09713 Human nit	Acf87485 Human SIR	Acn42845 Human dia	Aac67035 Human ind	Aax08434 Inducible	Aca56880 Human sig	Adi56676 Human pol	Adj74786 Marker ge	Adj74903 Marker ge	Aat98199 Human ind	Adq38958 Human SNP	Aaq66914 Seguence	Aat10115 Nitric ox	Aaa34818 Human ade
	ID	ADZ75764	AAH78096	AAH78095	ADV42931	ABX76286	ADA09713	ACF87485	ACN42845	AAC67035	AAX08434	ACA56880	AD156676	ADJ74786	ADJ74903	AAT98199	ADQ38958	AAQ66914	AAT10115	AAA34818
	DB	14	4	4	14	œ	σ	13	13	4	7	10	12	12	12	~	13	N	~	٣
	Query Match Length DB	258	1152	3462	3462	3855	3855	3855	3928	3946	4062	4062	4062	4062	4062	4070	4133	4145	4145	4145
de	Query Match	99.8	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7
	Score	257.6	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4
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Claim 1; SEQ ID NO 1; 13pp; English

Aaf20940 Human ind	Aah47966 Mouse ind	Aah47959 Human ind	Abz96634 Human ind	Abd19732 Human ind	Aaq77700 Nitric-ox	Adi32081 Human cDN	Ads84148 Human lym	Adq38959 Human SNP	Aeb69128 Human mod	Acn42844 Human dia	Acn42843 Human dia	Aaf21450 Human ind	Abz97144 Human nuc	Abd19730 Human ind	Aaa34820 Human ade	Aaf20942 Human low	Abz96636 Human nuc	Abd20500 Human pul	Aaf21436 Human enz	Abz97130 Human nuc	Abd17969 Human enz	Aac67036 Human ind	Ads88001 Tumour tr	Rat	Aaq79423 Rat induc
AAF20940	AAH47966	AAH47959	AB296634	ABD19732	AAQ77700		ADS84148	ADQ38959	AEB69128	ACN42844	ACN42843	AAF21450	ABZ97144		AAA34820	AAF20942	AB296636	ABD20500	AAF21436	ABZ97130	ABD17969	AAC67036	ADS88001	AAQ79418	AAQ79423
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4145	4145	4145	4145	4145	4164	4164	4164	4221	4221	4277	4278	8222	8222	8222	9513	9513	9513	9513	35384	35459	35459	4150	4150	1033	3530
46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.0	46.0	36.7	36.7
120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	120.4	118.8	118.8	94.8	94.8
20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ADZ75764 standard; DNA; 258 BP.

ADZ75764

ADZ75764;

ds; gene; high altitude pulmonary edema; pulmonary edema; respiratory-gen.; respiratory disease; SNP detection; allelic variation; Detecting predisposition to high altitude pulmonary edema (HAPE) by amplifying intron 7 of human inducible nitric oxide synthase gene, and predicting and analyzing differences in the distribution of allelic /*tag= a /standard_name= "single nucleotide polymorphism" Human inducible nitric oxide synthase gene exon 7 SEQ ID NO:1. (COUN-) COUNCIL SCI & IND RES INDIA. Location/Qualifiers 13-NOV-2003; 2003US-00713137 13-NOV-2003; 2003US-00713137. (first entry) Pasha AQM, Ahsan A; WPI; 2005-384299/39. US2005106573-A1 Homo sapiens. 19-MAY-2005. 28-JUL-2005 Key variation variants. exon.

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                                                                                                                                                                                                                                                                                                        GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                    9
           high altitude pulmonary edema (HAPE). The method comprises amplifying intron 7 of the human inducible nitric oxide synthase (INOS) gene (ADZ7574) by designing and synthesizing forward and reverse oligonucleotide primers (ADZ75765+ADZ75766), and predicting and statistically analyzing differences in the distribution of the allelic variants in the populations, where GG genotype at 19480 position are at low risk of HAPE, and AA genorype at 19480 position are at high risk of HAPE. The present sequence represents exon 7 of the human iNOS gene.
 invention relates to a novel method for detecting predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening for compounds that inhibit in vitro inducible nitrogen oxide synthase useful for treating organ rejection, cerebral infarction and
                                                                                                                                                                                                                                                                                                                                                                                                          ACAGAGTGGAGCCCAGAGGAGACACGCAGCCCGGGCTTACAGACTCACAGGGCCCGTTT
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                                                                                                                                                                                                                                                                                                                                                                                          ACAGAGTGGAGCCCCAGAGGAGACACGCAGCCCGGGCTTACAGACTCACAGGGCCCGTCTT
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of a human inducible nitrogen oxide synthase.
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                                                                                                                                                                  DB 14; Length 258;
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                                                                                                                                        Seguence 258 BP; 52 A; 80 C; 84 G; 41 T; 0 U; 1 Other;
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                                                                                                                                                                              .3e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         initrogen oxide synthase; iNOS; or infarction; vascular ischemia; ss.
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                                                                                                                                                                 Score 257.6;
Pred. No. 1.
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100.0%; Pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GITCCCCAGCTGTGCATC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH78096 standard; DNA; 1152 BP.
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                                                                                                                                                                                              Conservative
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                                                                                                                                                                              Local Similarity
les 258; Conserv
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                           inhibit in vitro inducible nitrogen oxide synthase (iNOS) activity. The method comprises contacting the iNOS monomer with a candidate compound, and selecting those compounds that bind to it. As dimerisation of iNOS is the final step of the acquisition of the iNOS enzymatic activity, iNOS inhibitor compounds can can be quickly and efficiently screened. The inhibitors are useful for treatment and prevention of organ rejection, cerebral infarction and vascular ischemia. The present sequence encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes a method of screening for compounds that inhibit in vitro inducible nitrogen oxide synthase (iNOS) activity. The method comprises contacting the iNOS annower with a candidate compound, and selecting those compounds that bind to it. As dimerisation of iNOS is
                                                                                                                                                                                                                                                                                               438
                                                                                                                                                                                                                                                                                                                               GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                               439 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        compounds that inhibit in vitro inducible nitrogen oxide il for treating organ rejection, cerebral infarction and
                                                                                                                                                                                                                                                                                                  CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
The specification describes a method of screening for compounds that inhibit in vitro inducible nitracen and a compounds that
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                                                                                                                                                                                                    Length 1152;
                                                                                                                                                                        Sequence 1152 BP; 275 A; 326 C; 322 G; 229 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inducible nitrogen oxide synthase; iNOS; organ rejection; cerebral infarction; vascular ischemia; 88.
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                                                                                                                                                                                                    Score 120.4; DB 4;
Pred. No. 2.6e-24;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of a human polypeptide.
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                                                                                                                                                                                                     46.7%;
99.2%;
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Best Local Similarity
Matches 121; Conserv
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                                                                                                                                                                                                                                                                                             864
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                                             rebral infarction and vascular ischemia. The present sequence was used the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microarray; psychoneuroendocrinimmune; chronic fatigue;
non-insulin dependent diabetes; allergy; immune disorder; inflammation;
cancer; neoplasm; infection; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                   GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGGACCCTGCCAACGTGGAATTCACTCAG
the final step of the acquisition of the iNOS enzymatic activity, iNOS inhibitor compounds can can be quickly and efficiently screened. The inhibitors are useful for treatment and prevention of organ rejection,
                                                                                                                                                                                                                    CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCGCTATGCT
                                                                                                                                                                                              1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                               Gaps
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                                                                                               Sequence 3462 BP; 801 A; 1027 C; 962 G; 672 T; 0 U; 0 Other;
                                                                                                                                                              Indels
                                                                                                                               DB 4;
                                                                                                                             46.7%; Score 120.4; DB 4 99.2%; Pred. No. 3.3e-24;
                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADV42931 standard; cDNA; 3462 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human psychoneuroendocrinimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                Best Local Similarity 99.2
Matches 121; Conservative
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polyneptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                   804
                                                                                                                                     GGCTACCAGATGCCAGATGGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
                                                                                         CAGCGGAGTGATGGCAAGCACGACTTCCCGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                     Gaps
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                                   Indels
 Score 120.4; DB 14
Pred. No. 3.3e-24;
); Mismatches 1;
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10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-039245P.
13-NOV-2001; 2001US-0350666P.
29-NOV-2001; 2001US-0334370P.
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46.7%;
                                                                                                                                                                                                                                                                                                                                  ABX76286 standard; DNA; 3855
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                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
 Query Match
Best Local Similarity 99.2
Matches 121; Conservative
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Sequence 3855 BP; 894 A; 1136 C; 1067 G; 0 T; 758 U; 0 Other;

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lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, librosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polymucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polymucleotides of the
                                                                                                                                                                                                                                                                                                                                 939 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 998
                                                                                                                                                                                                                                                                                                                                                                       GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to screening assays for testing nutraceuticals. The invention provides methods for detecting RNA in cells exposed to various types, concentrations, and combinations of nutraceuticals using the INVADER detection assay. The INVADER detection assay detects and quantifies test gene mRNA. The INVADER assay detection reagents comprise a probe and an INVADER oligonucleotide. The invention provides a high throughput, sensitive, quantitative, and cost-effective method of testing nutraceuticals. The present sequence represents human nitric oxide synthase 2A (NOS2A) mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Testing nutraceutical by providing cells, nutraceutical, and INVADER assay detection reagents, exposing cells to nutraceutical, lysing cells; and contacting cell lysate with INVADER assay detection reagents.
                                                                                                                                                                                                                                                                                          CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening assay; nutraceutical testing; mRNA detection;
INVADER detection assay; human; nitric oxide synthase 2A; NOS2A; ss.
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                                                                                                                                                                                                              Score 120.4; DB 8; Length 3855; Pred. No. 3.4e-24; 0; Mismatches 1; Indels 0;
                                                                                                                                                                         Sequence 3855 BP; 894 A; 1136 C; 1067 G; 758 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human nitric oxide synthase 2a (NOS2A) mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 2; 25pp; English.
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                                                                                                                                                                                                              46.7%;
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                                                                                                                                                                                                                                                    Conservative
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The invention relates to a novel method for in vitro detection of systemic inflammatory response syndrome (SIRS). The method comprises detecting abnormal expression of disease-related genes, or their associated peptides. The method of the invention demonstrates antibacterial, immunosuppressive and antiinflammacory applications and may be used for early differential disaposis, monitoring progression, assessing risk, assessing the likely response to treatment and for post mortem diagnosis of systemic inflammatory response syndrome, sepsis and sepsis like conditions. The recombinant or synthetic acid sequences of the invention, or derived proteins or peptides, may be useful as calibrants in assays for the specified diseases, for evaluating cutivity or toxicity in screening for active agents and/or for preparation of agents for treatment or prevention of the specified diseases. The current sequence is that of a human SIRS/sepsis diagnostic marker DNA fragment of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published
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                                                                                                                                                                In vitro detection of systemic inflammatory response syndrome and related conditions, for e.g. monitoring progression, comprises detecting abnormal expression of disease-related genes.
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                                                                                                                                           61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                                                           1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                       Gaps
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   Length 3855;
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                                     Indels
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DB 9;
 46.7%; Score 120.4; DB 9
80.3%; Pred. No. 3.4e-24;
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                                     23; Mismatches
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                                                                                                                                                                                                                                                                                                                                              ACF87485 standard; DNA; 3855 BP.
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08-AUG-2003; 2003DE-01036511.
02-SEP-2003; 2003DE-01040395.
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                     98; Conservative
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 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorder, autoimmune/inflammatory disorders, autoimmune/inflammatory disorders, gastrointestinal disorders, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence data for this patent is not represented in the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a novel method of treating influenza virus infection by administering an antisense oligonucleotide directed at the human inducible nitric oxide synthase (iNOS) mRNA. This is useful in preventing the symptoms of influenza infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; influenza virus; antisense; inducible nitric oxide synthase; iNOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating viral influenza with antisense oligonucleotides that hybridize with inducible nitride oxide synthase mRNA and inhibit synthesis of the enzyme, reducing the production of nitric oxide in lungs.
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                                                                                                                                                                                                                                                     directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                            DB 13; Length 3928;
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                                                                                                                                                                                                                                                                                        Sequence 3928 BP; 928 A; 1151 C; 1086 G; 763 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human inducible nitric oxide synthase coding sequence #1.
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Pred. No. 3.4e-24;
0; Mismatches 1; Indels
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99.2%;
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                                                                                                                                                                                                                                                                                                    998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
    oct sequences. Furthermore, a number of arbitrary SEQ ID NO.s are lisclosed within the specification, however, these have not been taken onto account during indexing due to inconsistencies in application and
                                                                                                                                                                                                                                                                                    1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                DB 13; Length 3855;
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                                                                                                                     Sequence 3855 BP; 897 A; 1134 C; 1065 G; 759 T; 0 U; 0 Other;
                                                                                                                                                                                                               Indels
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                                                                                                                                                                  Score 120.4; DB 13
Pred. No. 3.4e-24;
0; Mismatches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-2002; 2002US-0410259P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-2003; 2003WO-US028227
                                                                                                                                                                Query Match
Best Local Similarity 99.2%;
Matches 121; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GT 122
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850 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGAAATGCTCAGCTCATCCGCTATGCT 909
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antioxidising agent. The methods can be used for protecting cells against immunotoxicity mediated by, e. g. 1L-1 beta, 1L-1 alpha, gamma IFN, TNF alpha, TNF beta, 1L-8, IL-6, IL-1, IL-5, IL-7, IL-9, IL-14, IL-17, granulocyte-macrophage colony stimulating factor or monocyte chemoattractant protein-1. The methods can be used for the treatment of e.g. insulin-dependent diabetes mellitus (IDDM), NIDDM, obesity, wasting syndromes, short stature, osteoporosis, inflammatory diseases, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                             GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                       910 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signalling pathway population; cancer; adenocarcinoma; leukaemia; immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
                                                                                                                                                                                                                                                                                                                                         1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Combination of polynucleotide probes, useful as array elements in microarray for monitoring the expression of a number of target
                                                                                                                                                                                                       Sequence 4062 BP; 966 A; 1178 C; 1099 G; 819 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human signalling pathway polynucleotide probe SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probe; 88; array element; Parkinson's disease;
                                                                                                                                                                                                                                               46.7%; Score 120.4; DB 2;
99.2%; Pred. No. 3.4e-24;
tive 0; Mismatches 1;
                                                                                                                                                             diseases, or neurodegenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1478; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAS6880 standard; cDNA; 4062 BP.
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                                                                                                                                                                                                                                                                                             Conservative
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Best Local Similarity
Matches 121; Conserv
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ID ACAS
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                                                                                                                                                                                                       GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                              745 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manganese containing superoxide dismutase; MnSOD; IDDM; diabetres mellitus; treatment; therapy; nitric oxide; NO; beta cell; fatty acids; lipotoxic; cytocoxic; cytokine; osteoporosis; inflammatory disease; autoimmune disease; neurodegenerative disease; ss.
                                                                                                                 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                          Gaps
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                           Length 3946;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Newgard CB, Unger RH;
Lee Y;
                                                                        1; Indels
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                         Score 120.4; DB 4;
Pred. No. 3.4e-24;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 244-247; 253pp; English.
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Ohneda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inducible nitric oxide synthase gene.
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                         46.78;
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1, Koyama K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
         Query Match
Best Local Similarity 99.27
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Shimabukuro M,
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03-MAR-1998;
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monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunogathies e.g. AlDS and asthma, neuropathies e.g. Alzheimer's disease and Parkinson's disease. The present sequence represents a polymucleotide probe of the invention. Note: The sequence cata for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; probe; ss; receptor-like polypeptide; transducing polypeptide; effector-like polypeptide; cancer; immunopathology; neuropathology; drug development; toxicology; carcinogenicity; signalling pathway polypeptide; adrenal gland; bladder; bone; bone marrow; brain; breast; cervix; tumour; immunopathology; diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology; dementia; amnesia; epilepsy; Alzheimer's disease; depression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.7%; Score 120.4; DB 10; 99.2%; Pred. No. 3.4e-24; tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                             seqdata.uspto.gov/sequence.html?DocID=06500938B1
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Les 121; Conservative
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Claim 6; SEQ ID NO 1478; 73pp; English

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The invention relates to a composition of polynucleotide probes comprising first polynucleotide probes comprising at least a portion of a gene encoding a receptor-like polypeptide, second polynucleotide probes comprising at least a portion of a gene encoding a refeator-like polypeptide. The probes of the composition are useful as array elements in a microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the expression of target polynucleotides. The microarray is useful in the diagnosis and treatment of cancer, an immunopathology or a neuropathology. It can also be used for drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. Microarrays can also be used for monitoring the progression of diseases that may be associated with the altered expression of signalling pathway collypeptides. The composition can also be used to purify a subpopulation of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile collypeptides. The diagnosis and treatment of cancer, e.g. cancers of is also useful for the diagnosis and treatment of cancer, e.g. cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix, an immunopathology, e.g. AlDS, diabetes, pancreatitis, osteoporosis or ulcerative colitis, or a neuropathology, e.g. dementia, amnesia, chuman polymucleotide probe of the invention. Note: The sequence represents a chuman polymucleotide formed directly from USPPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bronchial asthma; chronic obstructive pulmonary disease;
respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
gene therapy; marker gene; gene; ds.
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46.7%; Score 120.4; DB 12; Length 4062;

Best Local Similarity 99.2%; Pred. No. 3.4e-24;

Matches 121; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4062 BP; 966 A; 1178 C; 1099 G; 819 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ74786 standard; DNA; 4062 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-AUG-2003; 2003EP-00254857.
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20-MAR-2003; 2003JP-00077212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENO-) GENOX RES INC.
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Best Local Similarity
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ADJ74786
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Homo sapiens, EP1394274-A2

03-MAR-2004

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The present invention describes a metrod of refering to concitat astimate or chronic observative pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a bablet, comparing the expression level determined with the expression level a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (51) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13, or (b) a group of genes (52) cells are stimulated with interleukin-13. Also described; (l) a reagent (l) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a cethma or chronic obstructive pulmonary disease, comprising the compound, a sethma or chronic obstructive pulmonary disease, comprising the compound, cobstructive pulmonary disease, comprising the compound, a sethma or chronic obstructive pulmonary disease, comprising for cobstructive pulmonary disease, comprising for cobstructive pulmonary disease, and can be used in gene therapy. The method cobstructive pulmonary disease, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent in vertice obstructive pulmonary disease. The present control is sequence is useful for testing for or screening for a therapeutic agent invention.
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respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
gene therapy; marker gene; gene; ds.
                                                                                                                                                                                                                                      present invention describes a method of testing for bronchial asthma
                                                                    for bronchial asthma or chronic obstructive pulmonary disease by
                                                                                     comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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0; Mismatches 1
                                                                                                                                                                                     Claim 1; SEQ ID NO 38; 241pp; English
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Matches 121; Conservative
                      WPI; 2004-193155/19
                                                                                                                                            healthy subject.
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                                                                       Testing
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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises or chronic obstructive pulmonary disease. The method comprises cor chronic obstructive pulmonary disease. The marker gene in a biological sample from a subject, comparing the expression level of the marker gene in a biological sample from a healthy comparing whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial colls are calls are stimulated with interleukin-13. or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (l) a reagent (l) for teating for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to trreat bronchial asthma or chronic obstructive pulmonary disease; (s) a manker gene or an immal model for bronchial asthma or chronic obstructive pulmonary disease, (compound, constructive pulmonary disease, compound, constructive pulmonary disease, comprising the compound, constructive pulmonary disease, comprising the compound, constructive gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding conting to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense marker gene, and (1) a DNA chip for testing for a protein encoded by a marker gene, and (1) a DNA chip for testing for a protein 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Izuhara K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamaya M,
                                                                                                                                                                                                                                                                                                                              06-AUG-2002; 2002JP-00229312.
20-MAR-2003; 2003JP-00077212.
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Matches 121, Conservative
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(first entry)

us-10-713-137-1.rng

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ADQ38958 standard; DNA; 4133 BP.
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Best Local Similarity
                                                                        18-NOV-2004
                                                  ADQ38958;
          RESULT 16
                   ADQ38958
                                        This cDNA sequence includes a coding region for human penis inducible nitric oxide synthetase (HPiNOS) (see AAM36113). It was isolated by reverse transcription of mRNA from human penile smooth muscle cells with iNOS antisense primers, combined with PCR amplification of the resulting cDNA fragments. The invention is directed to a method of treating cerectile dysfunction, and introducing an agent capable of treating erectile dysfunction, and introducing an effective amount of the agent into the penile tissue of the patient. Preferrably, the agent induces cavernosal smooth muscle relaxation, and/or produces an increase in the level of NOS in tissue. Preferably, the NOS is iNOS, and the agent is introduced into the corpora cavernosa of the penis. The agent is preferably an NOS inducer, an NOS protein such as HPINOS, a cDNA encoding an NOS such as HPINOS, or cDNA-transformed penile cells, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       941 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1000
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                                                                                                                                                                                                                                                                                                                                                              Treatment of erectile dysfunction - by introducing an agent into penile tissue, particularly for inducing cavernosal smooth muscle relaxation or increasing NOS levels.
                                                                                            Nitric oxide synthetase; NOS; iNOS; HPiNOS; human; erectile dysfunction; impotence; gene therapy; corpora cavernosa; relaxant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4070 BP; 947 A; 1197 C; 1112 G; 814 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 120.4; DB 2;
Pred. No. 3.4e-24;
0; Mismatches 1;
                                                                          Human inducible nitric oxide synthetase cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; Page 35-38; 53pp; English.
                                                                                                                                                Location/Qualifiers
197. .3658
/*tag= a
           AAT98199 standard; cDNA; 4070 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.7%;
                                                                                                                                                                                                                                                                                    GONZ/) GONZALEZ-CADAVID N F.
                                                                                                                                                                                                                                                              96US-0017373P.
                                                                                                                                                                                                                                        97WO-US007643
                                                      11-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 99.2
nes 121; Conservative
                                                                                                                                                                                                                                                                                                                  Gonzalez-Cadavid NF,
                                                                                                                                                                                                                                                                                                                                       WPI; 1998-008577/01
                                                                                                                                                                                                                                                                                               RAJF/) RAJFER J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1061 CT 1062
                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW36113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GT 122
                                                                                                                                                                                                                                         09-MAY-1997;
                                                                                                                                Homo sapiens
                                                                                                                                                                                               WO9742965-A1
                                                                                                                                                                                                                                                              10-MAY-1996;
                                                                                                                                                                                                                    20-NOV-1997.
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                                 AAT98199;
                                                                                               Nitric
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Matches
AAT98199
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The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an control acids comprises: an isolated nucleic acid molecule comprising at least to entry an include on the individual. The invention cut has specification or its complement and encoding any one of the amino comprising an amino acid sequence given in the specification; an isolated polymorphism of that specification or its complement and encoding any one of the amino comprising an amino acid sequence given in the specification; an antibody that specification and which is between about 16 and 1000 nucleotides in clargent, a kit for detecting an Sub given in the specification and which is between about 16 and 1000 nucleotides in clarge, a buffer and an enzyme; a method of detecting an SNP in a cut-olicity acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing or method is useful in identifying an individual who has an increased or method is useful in identifying an individual who has an increased or method is useful in identifying an individual who has an increased or composition for treating or preventing myocardial infarction. This composition for treating or preventing myocardial infarction. This sequence was not shown in the specification. The sequence has not shown in the specification; the MPDO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
Human SNP containing myocardial infarction-associated gene, SEQ ID 621.
                                                                                       Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4133 BP; 960 A; 1198 C; 1118 G; 840 T; 0 U; 17 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; SEQ ID NO 621; 145pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-2003; 2003WO-US040978.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (APPL-) APPLERA CORP
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                                                                                                                                                                                                                                                                                                                                          WO2004058052-A2
                                                                                                                                                                                                                                                       Homo sapiens.
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Length 4133;

Score 120.4; DB 13; Pred. No. 3.4e-24;

46.7%;

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951 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inducible nitric oxide synthase gene - useful in gene therapy to treat, e.g. vascular occlusive disease and cancer.
                                GGCTACCAGATGCCAGATGCCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
                                                                                                                                                                                                                                                                                                                                          Inducible nitric oxide synthase; iNOS; hepatocyte; gene therapy; vascular occlusive disease; cancer; infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Geller DA,
                                                                                                                                                                                                                                                                                                            Nitric oxide synthase cDNA clone pHINOS.
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
207. .3668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 72; Page 53-58; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nussler AK,
                                                                                                                                                                                                             AAT10115 standard; cDNA; 4145 BP.
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                                                                                                                                                                                                                                                                            (first entry)
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Matches 121; Conservative
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                                                                                                121 GT 122
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                                                                                                                                                                                                                                            AAT10115;
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                                                                                                               999 GGCTACCAGATGCCAGATGCCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 1058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ66914 is from human hepatocyte inducible nitric oxide synthase cDNA clone pHINOS from lambda Zap II CDNA library. The original source was induced human hepatocyte RNA. HINOS cDNA plasmid is pref. transformed in E. coli SOLN (ATCC 69126). The inventors claim a clone with the cDNA sequence in AAQ66914 and a cDNA clone which encodes AAR55764. The cloning and expression of a human tissue nitric oxide synthase CDNA provides a source of the enzyme for therapeutic purposes, for example to prevent the hypotensive shock seen with sepsis. (Updated on 25-MAR-2003 to correct PN
                                                                                            GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                              939 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 998
                                                                                                                                                                                                                                                                                                                                                                                          Sequence of the cDNA clone for human hepatocyte inducible nitric oxide
                              1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGCGGAGTGATGCCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA clone encoding human inducible nitric oxide synthase - used to prevent the hypotensive shock seen with sepsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Nitric oxide synthase; hepatocyte; hypotensive shock; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.7%; Score 120.4; DB 2; Length 4145; llarity 99.2%; Pred. No. 3.4e-24; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;
1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simmons RL;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Geller DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
207. .3668
/*tag= a
                                                                                                                                                                                                                                                                          AAQ66914 standard; cDNA; 4145 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93WO-US011401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92US-00981344.
                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nussler AK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYPI-) UNIV PITTSBURGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                         1059 CT 1060
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                                                                                                                                                           121 GT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ното варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
28-DEC-1994
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Matches 121;
                                                                                            61
                                                                                                                                                                                                                                                                                                          AAQ66914;
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Best Local
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RL;

Simmons

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1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
A cDNA clone (AAT10115), designated pHINOS, codes for the human obtained principle nitric oxide synthase (1NOS = AAR88464). It was obtd. by isolating mRNA from hepatcocytes induced in vitro for iNOS biosyntheeis, preparing a cDNA library in a phage lambda Zap II vector, and screening with a cross-species iNOS probe. The cDNA can be used to prepare iNOS for therapeutic use. Alternatively, it is used in gene therapy strategies for treatment of vascular occlusive disease associated with atherosclarosis, vascular bypass and diabetes mellitus, tumor cell growth, and microbial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            951 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCACCTCATCCTCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4145;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4145 BP; 968 A; 1205 C; 1124 G; 848 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 120.4; DB 2;
Pred. No. 3.4e-24;
0; Mismatches 1;
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us-10-713-137-1.rng

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The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets oncleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating c. graphaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD) and cancers such as leukaemias lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONS reduces of decoyadenosine which activates adenosine content of the correspond to sequence side effects. The A-containing ONS break down with the nucleotide sequences given in the sequence listing from the present to invention, which correspond to SEQ ID NO:1 to 1885, but the sequences of from the previously named sequences SEQ ID NO:1 to 1885, but the sequences given in the disclosure of the present invention. N.B. Sequences given in the disclosure of the present invention on the actuence given in the disclosure of the present invention on the sequence siven in the disclosure of the present invention on the parting tup with their corresponding SEQ ID No:1 to 185, but the sequence given in the disclosure of the present invention on the match
                                                                                                                                                                                                                                                                                                                                                                                                                       antiallergic, antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                       Human; adenosine receptor; low adenosine antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                              phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                      Human adenosine receptor related polynucleotide SEQ ID NO:2507,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 664-665; 1343pp; English.
                                                                                                                                                               AAA34818 standard; DNA; 4145 BP
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                                                                                                                                                                                                                                                             (first entry)
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                                              1071 CT 1072
121 GT 122
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                                                                                                                                                                                                                                                          28-JUL-2000
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                                                                                                                                                                                                                AAA34818;
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951 cadecadargaredeaageacaacartreeggrereagaargereagerearedeerarger 1010
                                                                                                                                                                                                           1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 1070
                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers
                                                                                                                                                                                         GGCTACCAGATGCCAGATGCCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors,
                                                                                                              1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human inducible nitric oxide synthase polynucleotide fragment #2507.
                                                                         ö
                                       Length 4145;
Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;
                                                                           Indels
                                       DB 3;
                                 Score 120.4; DB 3;
Pred. No. 3.4e-24;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 254-255; 1592pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       AAF20940 standard; DNA; 4145 BP.
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                                       46.7%;
99.2%;
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                                                                             Matches 121; Conservative
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                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                    121 GT 122
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chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, binding proteins, adenosine receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, cNS and peripheral nervous and non-nervous system peptide transmitters, defensine, growth factors, vassociated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiratory distrass syndrome (RDS), pain, cystic fibrosis (CP), allergic rhinitis (AR), pulmonary (NDS), pain, cystic fibrosis (CP), allergic rhinitis (AR), pulmonary hypertension, emphysems, chronic obstructive pulmonary disease (CDPD),
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                                                                                                                                                                                                                                                                                                 pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense oligonucleotide; inducible nitric oxide synthase; modilate expression; immunomodilator; antidiabetic; cardiovascular; cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury; 2.-0-methoxyethy1; phosphorothioate; mouse; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 46.7%; Score 120.4; DB 3; Length 4145; 99.2%; Pred. No. 3.4e-24; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;
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/product= "inducible nitric oxide synthase"
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207. .3668
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                               the present invention
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The invention relates to antisense compounds, especially oligonuclectides, which are targeted to a nucleic acid encoding inducible nitric oxide synthase and which specifically hybridise to and modulate expression of inducible nitric oxide synthase. The antisense compounds have immunomodulator, antidiabetic, cardiovascular, cardiant, neuroprotective, disorder and vasotropic activity. The antisense oligonuclectides are useful for inhibiting the expression of inducible nitric oxide synthase in cells or tissues. In particular, the antisense oligonucleotides are useful for inhibiting diseases or disorders associated with inducible nitric oxide synthase, e.g. diabetes, immunological disorder, cardiovascular disorder, neurological disorder or insorder, is cardiovascular disorder, neurological disorder or insorder, neurological disorder of monostile nitric oxide synthase (Genbank accession number M92649)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                New antisense oligonucleotides for modulating the expression of inducible nitric oxide synthase in cells or tissues, particularly useful for treating e.g. immunological, cardiovascular or neurological disorders, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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/product= "inducible nitric oxide synthase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 120.4; DB 4;
Pred. No. 3.4e-24;
0; Mismatches 1;
                                                                                                                                                          Example 13; Page 98-103; 144pp; English
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Best Local Similarity 99.2%;
Matches 121; Conservative (
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                  WPI; 2001-465340/50
                                 P-PSDB; AAG64498
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ischemia

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institution teraces to a invote phratmaceurial composition, which its a active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' or 3' end genomic flanking regions, continuations of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antinflammatory steroid and ubiquinone. A composition of the invention has antinflammatory, antiallergic, antiasthmatic, hypotensive, has antinflammatory, antiallergic, antiasthmatic, hypotensive, increasing or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antinflammatory steroid in a subject, for reducing or depleting levels of or or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of unginilammation, lung aurfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                          Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel pharmaceutical composition, which has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        951 caccegacidareccaaccaccacriccescrerecaarecreacticarecerrateer
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                                                                                                                                                      Pabalan J, Aguilar D;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 11876; 872pp; English.
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                                                                                                                                                         Katz B,
                                                                                                                                                                                     Tang L, Shahabuddin S;
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23-APR-2002; 2002WO-US013135.
                                                  24-APR-2001; 2001US-0286137P.
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                                                                                                          (EPIG-) EPIGENESIS PHARM INC
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Best Local Similarity 99.2
Matches 121, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                        New antisense oligonucleotides for modulating the expression of inducible nitric oxide synthase in cells or tissues, particularly useful for treating e.g. immunological, cardiovascular or neurological disorders, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for research and diagnostics. The present sequence is that of human inducible nitric oxide synthase (GenBank accession number L09210)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 4145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.7%; Score 120.4; DB 4;
99.2%; Pred. No. 3.4e-24;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                 Example 13; Page 92-97; 144pp; English.
                                                                                                             Cowsert LM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABZ96634 standard; DNA; 4145 BP.
     24-JAN-2000; 2000US-00490208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 121; Conservative
                                                          (ISIS-) ISIS PHARM INC
                                                                                                             Dean NM,
                                                                                                                                                                  WPI; 2001-465340/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CT 1072
                                                                                                                                                                                              P-PSDB; AAG64497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GT 122
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                                                                                                             CF,
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comprising oligonuclectides and the composition of the tribution describes and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, suffactant depletion or hyposecretion, when administered to a mammal. The oligonuclectides are derived from a gene encoding or regulating configuration or cancer and can be anti-sense to the corresponding mRNA.

Configuration or cancer and can be anti-sense to the corresponding mRNA.

The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonuclectides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antialersyle, antialfammatory, antiathmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a certarearchy or experience, immunosuppressive and cytostatic activity, is a certarearchy or experience, immunosuppressive and cytostatic activity, is a certarearchy or experience, immunosuppressive and cytostatic activity, is a certarearchy a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to ravailability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or bronchoconstriction and/or lung disease or condition such as pulmonary disease, pulmonary infections, the disease or condition such as pulmonary disease, pulmonary transplantation rejection, pulmonary infections, branchoconstriction, and/or bronchoconstriction and disease or condition such as pulmonary disease, pulmonary infections, branch content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the assets of the oligonucleotides into product the tite of the ol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention describes a novel composition (a) a first active agent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligonucleotide containing less percentage of adenosine, targeted unucleic acids associated with lung airway or lung dysfunction, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 4145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pharmaceutical composition for treating asthma, has antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.7%; Score 120.4; DB 1.99.2%; Pred. No. 3.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; SEQ ID NO 11876; 763pp; English,
                                                                                                                                                                                                                                                                                                                                                                                        Katz
                                                                                                                                                                                                                                                                                                                                                                                      Li Y, Sandrasagra A, K.
Tang L, Shahabuddin S;
                                                                                                                                                                                                                                             23-APR-2002; 2002WO-US013143
                                                                                                                                                                                                                                                                                          24-APR-2001; 2001US-0286036P.
                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bronchodilating agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-093058/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                  WO200285309-A2
                                                                                                     Homo sapiens.
                                                                                                                                                                                                 31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                            Miller S,
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                                                                                                                                                                                                                                                                                                                                                                                           Nyce JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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nitric-oxide-synthase. cDNA was generated and used to construct a library in lambda ZAPII. This was screened with a 650 bp fragment of mouse inducible NO-synthase cDNA to identify the full-length clone pBSHSINOS. The insert was transferred to pSVL to give a vector capable of expressing NO-synthase in CHO cells under control of a hererologous constitutive promoter. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                              Nitric-oxide-synthase; NO-synthase; NOS; chondrocyte; interleukin-1-beta; pBSHSINOS; arthritis; hypertension; septic shock; inflammation; ischemia; dementia; obesity; tumor; agonist; antagonist; vector; CHO; Chinese hamster ovary; cell culture; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human inducible nitric oxide synthase - useful for identifying enzyme inhibitors and stimulators, and for diagnosis and treatment of e.g. viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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99.2%; Pred. No. 3.4e-24;
live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 25-31; 42pp; English.
                                                                                                                                                                                       Nitric-oxide-synthase pBSHSINOS clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palmer RMJ;
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
226. .3687
/*tag= a
                                                                                         AAQ77700 standard; cDNA; 4164 BP.
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                                                                                                                                                             (first entry)
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Best Local Similarity 99.2
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Charles IG,
                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infections or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-333198/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAR63206
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                        1071 CT 1072
GT 122
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                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                     WO9423038-A1
                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-1993;
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                                                                                                                                              25-MAR-2003
09-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                13-OCT-1994
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121
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                                                                                                                      AAQ77700;
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                                                                                                                                                                                                                                                                                                                 Key
                                                                              AAQ77700
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1; Indels

0; Mismatches

Matches 121; Conservative

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The invention relates to a composition comprising a plurality of CDNAs for detecting the altered expression of genes in an immunological invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, contacting the treatment of an immunopathological condition in a sample, contacting the treatment of an immunopathological conditions to form one or more hybridisation complexes and comparing the levels of the detected in complexes with the level of hybridisation complexes with the level of hybridisation complexes with the level of hybridisation complexes orrelates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and comparing to the expression of target polymuclectides. The microarray for monitoring are useful as hybridisable array elements in a microarray for monitoring the diagnosis of an immunopathology, such as Crohn's disease, asthma, culcerative colitis, hypereosinophilia, irritable bowel syndrome, culcerative colitis, hypereosinophilia, irritable bowel syndrome, carcinogenicity studies, forensics or pharmacogenomics. The microarray may also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition may also be used in purification of a subpopulation of a finance comparing the parent of the disconse. The microarray may calso be used in purification of a subpopulation of a funds of the current of the the print of the diagnosic of the print of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
                                                                                                                                                                                                                                           Human; gene; ss; immunological response; immunopathological condition; Crohn's disease; asthma; ulcerative colitis; hypereosinophilia; irritable bowel syndrome; osteoarthritis; rheumatoid arthritis; acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer; osteopathic; antiarthritic; antirheumatic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4164 BP; 974 A; 1210 C; 1127 G; 853 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1407; 50pp; English.
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                                                 ADI32081 standard; cDNA; 4164 BP
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                                                                                                                                                   entry)
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                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-895307/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osteoarthritis.
                                                                                                                                                                                                  Human cDNA #1407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6607879-B1
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-FEB-1998;
                                                                                                                                                17-JUN-2004
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                                                                                                  ADI32081;
RESULT 26
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Score 120.4; DB 11; Length 4164; Pred. No. 3.4e-24;

46.7%;

Best Local Similarity

Query Match

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                                                                                      1030 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to polynucleotides which are used as probes to detect genes differentially expressed in an immunological response, abundantly expressed in an immunological response, polypeptide known to regulate blood cell biology. The polynucleotides are useful in research and diagnostic applications particularly in cancer and immunopathological conditions, such as AIDS, allergies, anneania, asthma, atherosclerosis, bronchitis, ulcertaive colitis, diabetes, multiple sclerosis, osteoporosis, pancreathis, infections and arthritis. The present sequence represents a human lymph node CNNA used to detect blood
                                 cell and immunological response gene expression. Note: The present sequence does not appear in the printed specification but was obtained in electronic format from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New compositions having a number of first, second and third polynucleotide probes, useful in research and diagnostic applications in cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
9
                                                                     GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
1 CAGCGGAGTGATGCCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                              ss; gene; human; immunological response; blood cell; cancer; immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis; bronchitis; ulcerative colitis; diabetes; multiple sclerosis; osteoporosis; pancreatitis; infection; arthritis; lymph node.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.7%; Score 120.4; DB 13; Length 4164; 99.2%; Pred. No. 3.4e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (segdata.uspto.gov/sequence.html?DocID=20040077003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seilhamer JJ;
                                                                                                                                                                                                                                                                     ADS84148 standard; cDNA; 4164 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-00023655.
                                                                                                                                                                                                                                                                                                                                                                                Human lymph node cDNA #1407.
                                                                                                                                                                                                                                                                                                                                            11-AUG-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cocks BG, Stuart SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                             1090 CT 1091
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                                                                                                                                            GT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infections
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                                                                                                                                                                                                                                                                                                           ADS84148;
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Query Match
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(NICO/)
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AEB69128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual the invention caltered risk for myocardial infarction in the individual the invention caltered risk for myocardial infarction in the individual. The invention the specification or its complement and encoding any one of the amino the specification or its complement and encoding any one of the amino cald sequences given in the specification; an antibody that specification and which is between about 16 and 1000 nucleotides in exament; a buffer and an enzyme a method of detecting an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the proportion and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and method in infarction. The novel detection method has cardiant activity. The nucleic acide of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or
                                                                                                        1030 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGGAATTCACTCAG 1089
                                    970 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1029
                                                                                  61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human SNP containing myocardial infarction-associated gene, SEQ ID 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myocardial infarction, detection, single nucleotide polymorphism, SNP, cardiant; gene therapy, human, gene, ds.
CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                                                                                                                                                                  ADQ38959 standard; DNA; 4221 BP.
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10-MAR-2003, 2003US-0453135P.
30-APR-2003, 2003US-0466412P.
23-SEP-2003, 2003US-0504955P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-533949/51.
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                                                                                                                                                                  GT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                          composition for treating or preventing myocardial infarction. This polymuclectide sequence represents a human myocardial infarction-associated gene containing one or more SNP's of the invention. Note: Thi sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modulating agents useful for diagnosing or treating, for e.g. cancer, comprises screening for agents that modulate the activity of a modifier
risk for developing myocardial infarction and for preparing
                                                                                                                                                                                                                                                                                                                                                                                                              1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1009 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                                                                                                                                 46.7%; Score 120.4; DB 13; Length 4221; 99.2%; Pred. No. 3.4e-24;
                                                                                                                                                                                                                      Sequence 4221 BP; 998 A; 1216 C; 1133 G; 857 T; 0 U; 17 Other;
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Jin Y,
                                                                                                                                                                                                                                                                                                                                                Indels
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, Hitz BC, Lickteig K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human modulator of IGFR pathway polynucleotide #5.
                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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12-MAR-2004; 2004US-0552634P.
21-JUN-2004; 2004US-0581696P.
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Matches 121; Conservative
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Adamkewicz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-582573/59.
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Claim 1; Page; 190pp; English.
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Stevens KA,
Peralta CH,
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Harthshorne
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Xu Y, Kwor
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agent, the system provides a reference activity and detecting a test agent-biased activity of the assay system, where a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate IGFR pathway modulating agent. The invention also relates to methods for modulating an IGFR pathway of a cell or in a mammallain cell and a method for diagnosing a disease in a patient. The methods are useful for diagnosing or treating cancer or for identifying modulators of an IGFR pathway, which may be utilized as therapeutic targets for disorders associated with defective IGFR function, such as polymucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Monosy EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Magrove J, Vitt UA, Kirton ES;
Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                           GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
                                                                                                                                                                                                                                       1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                 Query Match

46.7%; Score 120.4; DB 14; Length 4221;
Best Local Similarity 99.2%; Pred. No. 3.4e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                           Sequence 4221 BP; 1001 A; 1221 C; 1138 G; 861 T; 0 U; 0 Other;
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12-SEP-2002; 2002US-0410260P
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therappy. The human clasmostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or paraite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp polynucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gietzen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
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Norne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
EM, Delegemen AM, Pennear IS, Banville SC, Reddy TP;
S KA, Blanchard JL, Penzer SR, Wang X, Au AP, Gerstin EH;
A CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
S RB, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gletzel
S, Shi X, Suarez CJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 4277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4277 BP; 973 A; 1253 C; 1237 G; 814 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.7%; Score 120.4; DB 13
99.2%; Pred. No. 3.4e-24;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 99.2
Matches 121; Conservative
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99US-0127958P.

06-APR-1999; UYEC-) UNIV

EAST CAROLINA. J W.

WPI; 2000-679539/66.

Nyce JW; NYCE/)

24-MAR-2000; 2000WO-US008020

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A purpuleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine tutoimmune/inflammatory disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, the present sequence represents a dithp polynucleotide of the invention. Note: The sequence area for this patent is not represented in the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1348 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1408 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; human; airway disorder; bronchocolator; antifinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                     New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human inducible nitric oxide synthase polynucleotide fragment #3017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4278 BP; 972 A; 1253 C; 1238 G; 815 T; 0 U; 0 Other;
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0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.7%; Score 120.4; DB 13; 99.2%; Pred. No. 3.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF21450 standard; DNA; 8222 BP.
                                                                                                                                                                                                       Claim 1; Page; 190pp; English
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Matches 121; Conservative
                     WPI; 2004-329368/30.
P-PSDB; ABM84191.
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                                                                                                                                                               in gene mapping
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26-OCT-2000

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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense coligonucleotides the A is replaced by a 'Universal' or alternative base. (C) can have respiratory, bronchodiator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with cartivating peptide factors and malignancies, auch as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, immunoglobulins and antibodies, antibody receptors, cytokines and chemokine receptors, adenosine receptors, brinding proteins, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, bradykinin receptors, central nervous and non-nervous system peptide transmitters, defensins, growth factors, bradykinin respitators, central nervous and non-nervous system peptide cantisense oligonucleotides may be used in this way to treat disorders and receptors, brinding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders condition selected from pulmonary vasoconstriction, inflammation, allergic fibrosis (CP), pain, cystic fibrosis (CP), allergic rhinitis (AR), pulmonary conditions, emphysema, chronic obstructive pulmonary disease (CPDD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAFIRES are respected in the exemplification of fragment and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 1070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 8222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 252-254; 1592pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and respiratory obstructions.
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Matches 121; Conservative
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RESULT 34

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Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                        Human; antisense; lung dysfunction; nasal airway dysfunction; antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiatethmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                            Pabalan J, Aguilar D;
                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 12386; 872pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                             Katz E,
                                                                                                                                                                                                                                                              Sandrasagra A, Ka
, Shahabuddin S;
                                                                                                                                                                                          23-APR-2002; 2002WO-US013135.
                                                                                                                                                                                                                 24-APR-2001; 2001US-0286137P.
                                                                                                                                                                                                                                      (EPIG-) EPIGENESIS PHARM INC.
                     Human nucleic acid sequence
(first entry)
                                                                                                                                                                                                                                                             Li Y, Sar
Tang L,
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                                                                                                                                               WO200285308-A2.
                                                                                                                          Homo sapiens.
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17-0CT-2003
                                                                                                                                                                    31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                       ubiquinone.
                                                                                                                                                                                                                                                                       Miller S,
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a come in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine or receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8222 BP; 1731 A; 2574 C; 2360 G; 1557 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 120.4; DB 10; Length 8222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4e-24;
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0; Mismatches
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99.28;
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nes 121; Conservative
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                                                                  951 CAGCGGAGTGATGCCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
                                                                                                                  1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 1070
                                                                                                    120
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                                CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                    61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG
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respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
                                                                               Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
                                                                                                                                                                                                                                                                            Aguilar D;
                                                            Human inducible nitric oxide synthase DNA fragment 1897.
                                                                                                                                                                                                                                                                             Pabalan J,
                                                                                                                                                                                                                                                                             Katz E,
                                                                                                                                              pulmonary transplantation rejection; ds
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                                                                                                                                                                                                                                                                              Sandrasagra A,
                                                                                                                                                                                                                                                                                     Shahabuddin
       ABD19730 standard; DNA; 8222 BP.
                                                                                                                                                                                                                        23-APR-2002; 2002WO-US013143.
                                                                                                                                                                                                                                         24-APR-2001; 2001US-0286036P.
                                                                                                                                                                                                                                                            (EPIG-) EPIGENESIS PHARM INC
                                           (first entry)
                                                                                                                                                                                                                                                                                                       WPI; 2003-093058/08.
                                                                                                                                                                                                                                                                             Li Y, Sar
Tang L,
                                                                                                                                                                                    WO200285309-A2.
                                                                                                                                                                  Homo sapiens.
                                           29-JUL-2004
                                                                                                                                                                                                      31-OCT-2002.
                                                                                                                                                                                                                                                                                       Miller S,
                          ABD19730;
                                                                                                                                                                                                                                                                              Nyce JW,
ABD19730
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ţ Pharmaceutical composition for treating asthma, has antisense oligonucleotide containing less percentage of adenosine, targeted trucleic acids associated with lung airway or lung dysfunction, and bronchodilating agent.

Claim 15; SEQ ID NO 12386; 763pp; English.

curfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating configuration of the polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers; (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasthmatic, beta-adrenergic agonist. The composition of chearacting a respiratory, lung or malignant disease. The administered composition composition or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The requiremental polypeptide present in the lungs. The production and/or lung and present and present in the lungs. The polypeptide present in the lungs. inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiration, distress syndrome, pain, cystic fibrosis, allergic thinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system receptors, This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating. bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) recepto

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                                                                                                                                                                                                                                                                           1011 GCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 1070
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                                                                                                                                                                                                                                                GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, prevent any unwanted effects due to it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiallergic, antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; lachaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                             951 CAGCGGAGTGATGCCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                      1 CAGCGGAGTGATGCCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, adenosine receptor; low adenosine antisense oligonucleotide;
phosphorothioate; impaired respiration; inflammation; allergy;
allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                        0 U; 0 Other;
                                                                                             Length 8222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human adenosine receptor related polynucleotide SEQ ID NO:2509.
                                                                                                                                1; Indels
                                                                                         46.7%; Score 120.4; DB 11;
99.2%; Pred. No. 4e-24;
ive 0; Mismatches 1;
                                                      Sequence 8222 BP; 1731 A; 2574 C; 2360 G; 1557 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 666-669; 1343pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA34820 standard; DNA; 9513 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                121; Conservative
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                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA34820;
                                                                                                                                                                                                                                                61
                                                                                           Query Match
Best Local
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                                                                                                                                Matches
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impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, outsinomary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONS reduces side effects. The A-containing ONS break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1860 (AAA32323 to AAA3392) are specifically claimed ONS from the present invention. N.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2242 cagcggagtgarggcaagcacaacrrccaggrgragaargcrcagcrcarccacrargcr 2301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                                                                                                                                                                                                                                    Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 9513;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human low adenosine antisense oligonucleotide #2509.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                        46.7%; Score 120.4; DB 3; 99.2%; Pred. No. 4.1e-24; iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF20942 standard; DNA; 9513 BP
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J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2362 CT 2363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GT 122
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(NYCE/) NYCE
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                                                                                                                                                                                                                                                                                                            Listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 36
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WPI; 2000-679539/66

24-APR-2001; 2001US-0286137P. 23-APR-2002; 2002WO-US013135

WO200285308-A2 Homo sapiens.

31-OCT-2002

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The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense coligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodiator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with capturing peptide factors and malignancies, such as stimulating and cerivating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, addenosine receptors, cytokine and chemokine receptors, adenosine receptors, pradykinin receptors, central cerosus system (CNS) and peripheral nervous and non-nervous system creceptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction) and/or bronchoconstriction) and/or lung inflammation, allergy (ies) and/or surfactant hypoproduction which are associated with a disease or surfactant hypoproduction which are associated with a disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2242 cagcegagrearegeaageaceactrecegereregaarecreaecreatecreares 2301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCTACCAGATGCCAGATGCCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
             Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; antimense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchodination; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (RA), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.7%; Score 120.4; DB 3 99.2%; Pred. No. 4.1e-24;
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                                                                                                                        Disclosure; Page 737-739; 1592pp; English.
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Best Local Similarity 99.2
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the present invention
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entitlenamatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or mallignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of demosine or receptor, producing bronchodilation, increasing levels of adenosine creeptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition. Once: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO cat fitp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2302 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 2361
                                                                                                                                                                                                                                                                                                                       Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                           Pabalan J, Aguilar D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9513 BP; 2107 A; 2869 C; 2671 G; 1866 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 120.4; DB 10; Length 9513;
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4.ae-24;
4.ae-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.7%; Score ... 99.2%; Pred. No. 4.1e-.
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 11878; 872pp; English.
                                                                                                                                                                                                                               Katz E,
                                                                                                                                                                                                                                                  Tang L, Shahabuddin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABD20500 standard; DNA; 9513 BP.
                                                                                                                                                                                                                               Sandrasagra A,
                                                                                                                                                                                         (EPIG-) EPIGENESIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 121; Conservative
                                                                                                                                                                                                                                                                                        WPI; 2003-229219/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2362 CT 2363
                                                                                                                                                                                                                               Li Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GT 122
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                                                                                                                                                                                                                               Nyce JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 38
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analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ds. Human, antisense, bronchoconstriction; allergy, hyposecretion; pain, respiratory tract inflammation; adenosine sensitivity; lung, cancer; surfactant depletion; antiallergic, antilnflammatory; antiasthmatic; WO200285309-A2 Homo sapiens.

31-OCT-2002.

23-APR-2002; 2002WO-US013143.

24-APR-2001; 2001US-0286036P.

(EPIG-) EPIGENESIS PHARM INC

Aguilar D; Pabalan J, Katz E, Li Y, Sandrasagra A, Ka Tang L, Shahabuddin S; Nyce JW, L Miller S,

WPI; 2003-093058/08.

Pharmaceutical composition for treating asthma, has antisense oligonuclectide containing less percentage of adenosine, targeted trucleic acids associated with lung airway or lung dysfunction, and bronchodilating agent.

Claim 15; SEQ ID NO 11893; 763pp; English.

This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating comprising oligonucleotides, effective for alleviating comprising oligonucleotides, readiction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The colsonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung expression or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention as antiallergic, antialfammatory, antianthmetic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the amount of target polypeptide present in the lungs. The composition and/or bronchoconstriction and/or lung inflammation, allergies and/or bronchoconstriction and/or bronchoconstriction, and/or bronchoconstriction, respiratory clintlammation, allergies asthma, impeded respiration, respiratory transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to the composition are the administry content of the anti-sense oligos corresponding to the continue present in the target RNA serves to prevent the breakdown of the charget polyment of prevent the breakdown of the condition serves to prevent the breakdown of the condition are serves to prevent the breakdown of the condition are serves to prevent the breakdown of the condition are prevent or prevent the breakdown or conditions are associated to the

the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to e.g., lung, brain, heart, kidney, etc, prevent any unwanted effects due to it

Sequence 9513 BP; 2107 A; 2869 C; 2671 G; 1866 T; 0 U; 0 Other;

ö / Match 46.7%; Score 120.4; DB 11; Length 9513; Local Similarity 99.2%; Pred, No. 4.1e-24; nes 121; Conservative 0; Mismatches 1; Indels 0; Query Match Best Loca Matches

1 CAGCGGGAGTGATGGCAAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT

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AAF21436 standard; DNA; 35384 BP.

(first entry) 14-MAR-2001

AAF21436;

Human enzyme-related antisense polynucleotide #3003.

Low adenosine antisense oligonucleotide, phosphorothioate, allergy, human; airway disorder; bronchoconstriction; lung inflammation; bus surfactant depletion; respiratory, bronchodilator; antinflammatory; immunosuppressive; antiathmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; 88

Homo sapiens.

WO200062736-A2

26-OCT-2000

24-MAR-2000; 2000WO-US008020.

99US-0127958P. 06-APR-1999;

EAST CAROLINA. (UYEC-) UNIV

(NYCE/) NYCE J W.

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

Disclosure; Page 47-55; 1592pp; English.

oligonuclectides the A is replaced by a 'Universal' or alternative base oligonuclectides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antinfilammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and mallghancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodise, antibody receptors, cytokines and chemokine receptors and transmitters and non-specific enzymes, binding proteins adhesion molecules and their receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide receptors, readykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide transmitters, defensine, growth factors, vascutive applieds and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders The present invention describes low adenosine (A) content antisense

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and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or autactant hypoproduction which are associated with a disease or condition selected from pulmonary vascenstriction, inflammation, allergy from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAPI8434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
                                                                                                                                                                                                                                                                                                                                                                                      1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                                                                                                                                                   Length 35384;
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                                                                                                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                                                                                          Query Match
46.7%; Score 120.4; DB 3.
Best Local Similarity 99.2%; Pred. No. 5.5e-24;
Matches 121; Conservative 0; Mismatches 1:
                                                                                                                                                                                                                   the present invention
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Human; antisense; lung dysfunction; nasal airway dysfunction; antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. ABZ97130 standard; DNA; 35459 BP. Human nucleic acid sequence. (first entry) 17-0CT-2003 ABZ97130;

RESULT 40

Pabalan J, Aguilar D; Sandrasagra A, Katz E, L, Shahabuddin S; 23-APR-2002; 2002WO-US013135. 24-APR-2001; 2001US-0286137P. (EPIG-) EPIGENESIS PHARM INC Li Y, Sar Tang L, WO200285308-A2 31-OCT-2002 Nyce JW, Homo

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid WPI; 2003-229219/22. ubiquinone. Miller S,

or

Disclosure; SEQ ID NO 12372; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has

first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising and/or continiflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an attisflammatory steroid in a subject, for reducing or depleting levels of or ecceptor, producing bronchodilation, increasing levels of adenosine corrector, producing bronchodilation, increasing levels of adenosine corrector, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject, stissue, or treating bronchoconstriction, currently surfactant in a subject, so transcript disease or condition. Note: The sequence data for this patent is not represented in the printed set the with in the printed of 28247 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG Gaps Sequence 35459 BP; 7025 A; 10160 C; 10041 G; 7897 T; 0 U; 336 Other; DB 10; Length 35459; ö Indels CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCT Score 120.4; DB 10; Pred. No. 5.5e-24; 0; Mismatches 1; at ftp.wipo.int/pub/published_pct_sequences 46.78; Matches 121; Conservative Local Similarity 28308 CT 28309 GT 122 H 121 Query Match ò 셤 Š g ð 셤

Search completed: December 13, 2005, 16:32:42 Job time : 476 secs

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AX077896 Mus muscu CF744130 UI-M-GV0-CX385985 JGI XZT65 BP178167 BP178167 AZ044226 RPCI-23-3 DQ045247 Homo sapi BJ088070 BJ088070 AL125658 Fugu rubr DQ045248 Pan trogl CK016997 AGENCOURT BU425320 603961089 DR123141 49091370 DN757217 GL-CF-140 AJ334075 AJ394075 CV459880 UI-M-HB0-BJ733387 BJ733387 AL053013 Drosophil CA090625 SCSGAMZ10 CCS70671 AGENCOURT AX185276 Mus muscu BX919466 BX919466

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2994 bp DNA linear GSS 02-JUN-2005
Homo sapiens NOS2A gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominides, Homo.

1 (Dases 1 to 2994)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
Chimpanzees
Cer. PLoS Biol. 3 (6), E170 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Charges 1 to 2994)

Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.
Nielsen, R., Bustamante, C., Tänenbaum, D.M., Civello, D.,
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="taxon:9606"
/chromosome="17"
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BA008070
BA008010157
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/gene="NOS2A"
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Homo sapiens
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                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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AW65410 103369 MA
AQ800595 HS_5314_B
AQ720606 HS_5542_B
CC520102 CH240_367
AY419784 Homo sapi
CG668876 OST465233
CG506126 OST55467
AY419786 MMS muscu
BC083183 MMS muscu
BC083183 MMS muscu
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CG550955 OST410927
CF251860 hdm005_C0
BU125423 603151629
AL125664 Fugu rubr
AZ231351 RPCI-23-8
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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258
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gb_htc:*
gb_est5:*
gb_est5:*
gb_est7:*
gb_gs81:*
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ALIGNMENTS

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Gaps

Query Match
Best Local Similarity 99.2%; Pred. No. 6.7e-21;
Matches 121; Conservative 0; Mismatches 1; Indels 0;

locus_tag="HC15370"

ORIGIN

AL125676 Fugu rubr AQ095690 HS 3017 A BQ551961 H4012E11-

892 581 621 581 520

72.8

69.8 67.4 64.4

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AQ214630
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Pan troglodytes NOS2A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
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                                   Hominidae, Pan.

I (bases 1 to 2994)

Nielsen, K., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fladel-Alon, A., Tanenbaum, D.M., Civello, D.,
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

A Can for Positively Selected Genes in the Genomes of Humans and

Chimpanzees

(er) PloS Biol. 3 (6), E170 (2005)
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                                                                                                      805 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 864
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Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA.
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   745 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGGAATGCTCAGCTCATCGCTATGCT
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/locus_tag="HC15370"
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Pan troglodytes
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DQ047445.1 GI:66900644
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AQ214630
HS_3117_A1_F08_T7 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3117 Col=15 Row=K, genomic survey
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1 (Bases I to 453)
Mahairae, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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103369 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
AW654110
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
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/db_xref="taxon:9606"
/clone="Plate=3117 Col=15 Row=K"
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Plate: 3117 row: K column: 15
Class: BAC ends
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Location/Qualifiers
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AUTHORS
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Jniversity of Washington
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hes 100; Conserv
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AQ720606/c
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KEYWORDS
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AQ800595.1 GI:5717850
                                                                                                                      USDA, ARS, US MET Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
Emails sequencing. Bases called and alt_trimmed with phred
v0.980994.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae; Homo.
1 (bases 1 to 523)
Mahairas, G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
11282978
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Wector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1; Library made from pooled tissue From lymph node, ovary, fat, hypothalamus, and pituitary."
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10449764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Indels
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High Throughput Sequencing Center
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Pred. No. 8.5e-17;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
/mol type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                      BACKWARD: GTTTTCCCAGTCACGACG
Plate: 95 rows. L. column:
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                   PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
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Homo sapiens
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/clone lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
ECORI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
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1 (bases 1 to 518)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mahairas,G.G., Wallace,J.C., Smith,K., Zhao,S., Adams,M.D. and
Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ720606
HS 5542 B1 H02 T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic_clone Plate=1118 Col=3 Row=P, genomic survey sequence.
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401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Emax: (206) 616-3887
Emax: (206) 616-3887
Emax: (206) 616-3887
Clones are derived from the human BAC library RPCI-11. For BAC Clones are derived from the human BAC library availability, please context Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 890 row: H column: 2
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: jwallaceeu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGGAATGCTCAGCTCATCCGCTATGCT
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University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-3618
Fax: (206) 616-3618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .523
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="texon:9606"
/clone="Plate=890 Col=2 Row=H"
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High quality sequence stop: 523.
Location/Qualifiers
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E 1 (bases 1 to 842)
S Holt, R. Stott, J. Yang, G., Barber, S., Smailus, D., Prabhu, A.-L., Butterfield, Y., Kirkpatrick, R., Liu, J., Glann, T., Mayo, M., Chiu, R., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W., Dalrymple, B.P. and Tellam, Tellam, S., Barris, W., Chiu, R., Chiu, Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398 Contact: Rob Holt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing the British Columbia Cancer Agency Genome Science Centre 600 W 10th Ave, Vancouver, British Columbia, Canada V52 4E6 Tel: 604-877-6085

Fax: 604-877-6085

Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACRAR Resources
(http://www.chori.org/bacpac/codering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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CH240 367118.T7 CHORI-240 Bos taurus genomic clone CH240 367118, genomic survey sequence.
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(pieter@dejong.med.buffalo.edu). Clones may be purchased from AscPaC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.3%; Score 93.6; DB 9; Length 518; 95.0%; Pred. No. 5.8e-14; ive 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                  /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=1118 Col=3 Row=P"
                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                   Plate: 1118 row: P column: 3
Seg primer: T7
Class: BAC ende
High quality sequence stop: 518.
Location/Qualifiers
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CC520102.1 GI:31838390
                                                                                                                                                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                         FEATURES
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence as made by sequencing genomic exons and ordering them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3437 bp DNA linear GSS 17-DEC-2003
VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae, Homo.

1 (bases 1 to 3437)

1 (Lark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                              /cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBACI.3; Site_1: Mbo1; Site_2: Mbo1;
Hareford bull 11. Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   471 CAGAGGACCGACGCCAAGCACGACTTCCGCGTTTGGAACTCCCAACTCATCCGCTACGCT
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
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Columbia Genome Sciences Centre, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 90.2; DB 9;
Pred. No. 4.9e-13;
0; Mismatches 33;
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                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="breed: Hereford"
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/clone="CH240_367118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                              Location/Qualifiers
1. .842
/organism="Bos taurus"
                        column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GTACCCGGCCCAGCCTCAGCCRC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   591 GTAGGCGCCCCCCCCCTCCCCC 613
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1. .3437
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ilarity 76.9%;
Conservative
                                                                                                                                                                                                                                                                                                /sex="Male"
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Homo sapiens
                      Plate: 367 row: I
Seg primer: T7
Class: BAC ends.
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Best Local Similarity
Matches 110; Conserv
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OST55467 Mus musculus 1298v/Ev Mus musculus cDNA clone OST55467,
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2 (Dasses 2 to 526)
2 (Dasses 3 to 526)
2 (Dasses 4 to 526)
2 (Dasses 4 to 526)
2 (Dasses 4 to 526)
3 (Dasses 5 to 526)
3 (Dasses 6 to 526)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                    GGCTACCAGATGCCAGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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Pred. No. 1.2e-09;
0; Mismatches 28; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .526
/organism="Mus musculus"
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/clone="OST55467"
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/strain="129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.9%;
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AUTHORS
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CG506126
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Zambrowicz, B.P., Abuln, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, B.C., Edwards, J., Finch, R.A.,
Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Friddle, C.J., Gupta, P., Kohlhauff, B., Ma, Z., Q., Markesich, D.,
Payne, R., Detter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Zhu, Q., Person, C. and Sands, A.T.
Payne deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
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0
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/clone_lib="Mus musculus 129Sv/Ev"
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Best Local Similarity 77.0%; Pred. No. 1.2e-09;
Matches 94; Conservative 0; Mismatches 28;
                                                                                                                              Score 78.2; DB 10;
Pred. No. 8.7e-10;
0; Mismatches 28;

    .486
    /organism="Mus musculus"

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/db_xref="taxon:10090"
<1. .>3437
/gene="NOS1"
/locus_tag="HCM7006"
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GSS.
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                                                                                                                                       Query Match 30.3%;
Best Local Similarity 77.2%;
Matches 95; Conservative
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ORGANISM
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VERSION
KEYWORDS
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AUTHORS
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     gene
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CG668876
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Email: cgapbe-rement: n.h.gov
Tissue Procurement: Dr. James Lin, University of Iowa
Tissue Procurement: Dr. James Lin, University of Iowa
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_magemhgri.nih.gov
Akhter.N., Ayele.K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakealey,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.B., Bromstein, M.J., Ubdin, T.B., Tobhiyuki, S., Carninci, P., Prange, G., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hullyk, S.W., Villalon, D.K., Muzny, D.M., Sodargen, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Young, A.C., Shevchenko, Y., Bouffard, G.G. Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.T., Skalska, U., Smailus, D.E., Schnerch, A., Scholin, J.E., Jand Marra, M.A., Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 176 Row: o Column: 2 Stries: IRAK Plate: 176 Row: o Column: 2 passed the following selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6724320 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (24-582-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/lab_host="DH10B"
/note="Vector: pYX-ASC"
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/organism="Mus musculus"
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/clone="IMAGE:30533636"
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/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 5622)
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   AY419786 3420 bp DNA linear GSS 17-DEC-2003
Mus musculus NOS1 gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence as made by sequencing genomic exons and ordering them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     553 CAAAGGACTGATGCCAAGCATGACTTCCGAGTGTGGAACTCGCAGCTCATCCGCTATGCC 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               613 GGCTACAAGCCAGATGGCTCTACCTTGGGCGATCCAGCTAATGTGGGGGTTCACAGAG 672
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Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.
                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Giurognathi, Muroidea, Murinae, Mus.

1 (Dases 1 to 3420)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferridera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 1.6e-09;
0; Mismatches 28
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    .3420
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    /mol_type="genomic DNA"
    /db_xref="taxon:10090"

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Location/Qualifiers
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Mus musculus
                                                                  genomic survey sequence.
                                                                                                                  AY419786.1 GI:39775743
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1 Similarity 77.0%;
94; Conservative (
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요 ò 원 8 8 ö

Gaps

9

Gaps

DEFINITION

RESULT 13 BC066101

8 ð 유

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence as made by sequencing genomic exons and ordering them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AY419785 3430 bp DNA linear GSS 17-DEC-2003 Pan troglodytes NOS1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic_survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1920 GGCTACAAGCAGCCAGATGGCTCTACCTTGGGCGATCCAGCTAATGTGGAGTTCACAGAG 1979
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L bases 1 to 3430)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Territera, S., Wango, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, White, T.J., Sninsky, J.J.,
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 5626;
This clone has the following problem: frame shifted.
Location/Qualifiers
1. .5626
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Score 77.2; DB 4;
Pred. No. 1.7e-09;
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    .3430
    /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"

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                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:30533636"
/clone=ITMAGE:30533636"
/clone=Ithe="NH BMAP_GIO"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                   /note="Vector: pYX-ASC"
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Location/Qualifiers
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Pan troglodytes
                                                                                                                     /mol_type="mRNA"
/strain="C578L/6"
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Sciurognathi; Murcidea; Muridae; Mus.

1 (bases 1 to 5626)

Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Altschul, S.F., Zeeberg, B. Buetcow, K.H., Schemen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B. Buetcow, K.H., Schemen, C.M., Habh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Staplecno, M., Soares, M.B., Bonaddo, M.F., Casarant, T.L., Scheetz, T.E., Brownstein, M.J., Usdid, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Willalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerder, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schein, J.E., Jones, S.J. and Marra, M.B.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6724320
                                                                                                                                                                                                                                                                                                                               5626 bp mRNA linear HTC 24-FEB-2004 museulus nitric oxide synthase 1, neuronal, mRNA (cDNA clone BC066101
                                                                            1920 GGCTACAAGCCAGCCCAGATGGCTCTTGGGCGATCCAGCTAATGTGGAGTTCACAAG 1979
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Whe Bite: http://genome.uiowa.edu
Contact: bento-sc/genome.uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,B., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Will-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Trissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
                                           GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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Submitted (02-PEB-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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Mus musculus
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REFERENCE AUTHORS TITLE JOURNAL

REMARK COMMENT

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JOURNAL
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                     RESULT 16
CF251860
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E 1 (bases 1 to 540)

S Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Friddle, C.J., Gupta, A., Hannsen, G., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hannsen, G., Hu, Y., Huang, W., Jaing, C., Rey, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.

Whil kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
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                                                                                                                                                                                                                                                                                      CG650955 540 bp mRNA linear GSS 02-OCT-2003
OST410927 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST410927,
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Location/Qualifiers
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
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     Length 3430;
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Score 76.8; DB 10; Length
Pred. No. 2e-09;
0; Mismatches 27; Indels
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/clone_lib="Mus musculus 1295v/Ev"
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/mol_type="mRNA"
/strain="1295v/Ev"
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/clone="OST410927"
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                                                                                                                                                                                                                                                                                                                           mRNA sequence.
CG650955
CG650955.1 GI:37474804
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 Query Match 29.8%;
Best Local Similarity 77.5%;
Matches 93; Conservative
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820 bp mRNA linear EST 07-AUG-2003
hdm005_c06 LPS-activated macrophage cell line Gallus gallus cDNA,
CP251860
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
Curr. Simon Hubbard
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603151629F1 CSEQCHL19 Gallus gallus cDNA clone ChEST15918 5', mRNA
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                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria, Aves: Neognathae; Galliformes; Phasianidae, Phasianinae; Gallus.

1 (bases 1 to 820)
Wittzell,H., Bed'Hom,B., Morin,V., Young,J.R., Whittaker,C.J., Chausse,A.M. and Zoorob,R.
A collection of chicken ESTS from activated immune cells Unpublished (2003)
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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/mol_type="mRNA"
/db_xref="teaxon:9031"
/db_line="HD11"
/coll_line="HD11"
/clole_lib="LPS-activated macrophage cell line"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 rue Guy Moquet, BP 8, 94
Tel: 33 1 49 58 35 00
Fax: 33 1 49 58 33 81
Email: zoorob@vjf.cnre.fr.
                                                                                                                                                        CF251860.1 GI:33485115
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Gallus gallus
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Gallus gallus
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UPR 1983
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621 bp DNA linear GSS 14-JUN-2000
Mus musculus genomic clone RPCI-23-82G23,
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Akao,S., Nierman, F., Reldblyum,T., Malek,J., Shatsman,S.,
Akinrel,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
Jong,P. and Fraser,C.M.
Whouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-82G23.TV
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Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 82 row: G column: 23
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Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB. UK Email: biohelp@dmp.mrc.ac.uk Vector: pBluescript II KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCTATGCT
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                               Score 72.8; DB 11; Length 581;
Pred. No. 1.8e-08;
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The Institute for Genomic Research
This Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0200
Fax: 301 838 0208
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    .581
    /organism="Takifugu_rubripes"

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                                                                                                                                                                                                                                                                         /mol_type="genomic_DNA"
/db_xref="taxon:31033"
/clone="064007cF12"
/clone_lib="cosmid_064007"
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Mus musculus
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Best Local Similarity
                                                                                                V type: phe
PRIMER: KS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="CSEQCHL19"
/note="Organ: liver; Vector: pBluescript II KS(+); Site 1:
EcoRI; Site 2: Not1; Modification of pBluescript II KS(+)
EcoRI; Site 2: Not1; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3;
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BsgI and
BamHI sites [5'ggcggggagccccgggatcggaacagaagaag]
[5'aattcttttttcggatccgggctgcaccg]"
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Umrania,Y., Williams,G. and Brenner,S.
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Fugu rubripes GSS sequence, clone 064007cF12, genomic survey
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              of Biomolecular Sciences of Manchester Institute of Science and Technology
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ilarity 75.4%; Pred. No. 9.1e-
Conservative 0; Mismatches
                                                                                                                                                                                                                                      /mol type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="ChEST15918"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fugu rubripes by sequence scanning
Genome Res. 9 (10), 960-971 (1999)
                                                                               PO Box 88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                   organism="Gallus gallus"
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GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
                                                                                                Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               /sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
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Best Local Similarity
Matches 92; Conserv
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                                       University
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FR0038163
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Hominidae; Homo.

1 (bases 1 to 470)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ095690 470 bp DNA linear GSS 27-AUG-1998
HS_3017_Al_F08_MR CIT Approved Human Genomic Sperm Library D Homo
Bapiens genomic clone Plate=3017 Col=15 Row=K, genomic survey
                                                                                                                                                                                                                                                                                          GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                    320 GGGNACAAACAGCCTGATGGTCAGATCNTGGGGGACCCTGCTAATGTTGAATTTANTGAG 261
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH108"
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
                                                                                                            Length 581;
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                          Score 69.8; DB 11;
Pred. No. 1.1e-07;
0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="Plate=3017 Col=15 Row=K"
                    /clone="064007cE10"
/clone_lib="cosmid 064007"
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/db_xref="taxon:9606"
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Class: BAC ends
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/db_xref="taxon:31033"
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AQ095690.1 GI:3463425
                                                                                                            Query Match
Best Local Similarity 71.8%;
Matches 89; Conservative
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                                                                                                     /Bex="Pemale"
/lab host="DH10B"
/clone_lib="RPCI-23"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation and analysis of 25 Mb of genomic DNA from the pufferfish Fugu rubripes by sequence scanning Genome Res. 9 (10), 960-971 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FR0038175 581 bp DNA linear GSS 25-FEB-2004 Fugu rubripes GSS sequence, clone 064007cE10, genomic survey
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Blgarf.G. (Dlark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K.,
Unrania,Y. Williams,G. and Brenner,S.
Direct Submission
Submisted (11-OCT-1999) MRC Human Genome Mapping Project Resource
Centre, Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
Vertor: pApagemid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 CTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTG
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Pred. No. 9.7e-08;
1; Mismatches 26;
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL125676.1 GI:6107291
SGS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
organism="Mus musculus'
                    /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-82G23"
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77.4%;
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Best Local Similarity
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/tissue type="whole brain"
/dev stage="embryo 18.5 dpc"
/lab.host="DH108 (TI phage resistant)"
/done lost="DH108 (TI phage resistant)"
/clone lost="MIH BMAP EH0p"
/clone lost="Organ: brain".Vector: pYX-Asc; Site_1: EcoR I;
/clone lost="Organ: brain".Vector: pYX-Asc; Site_1: EcoR I;
/clone lost="Organ: brain".Vector: pYX-Asc; Site_1: EcoR I;
/site_2: Not I; The library was constructed according to
Bonalo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
gel: First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is CAGCCACGAC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institute of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator:"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L Unpublished (1999)

L Unpublished (1999)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin, Univeristy of Iowa

CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

CONA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

CONE Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

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CONE Arrayed by: Dr. M. Bento Soares

CONE Arrayed by: Dr. M. Brento Soares

CONE Arrayed by: Dr. M. Br
                                                                                                  BM950581 711 bp mRNA linear EST 14-MAR-2002 UI-M-EHOp-buu-d-15-0-UI.rl NIH BMAP_EHOp Mus musculus cDNA clone IMAGE:5687006 5', mRNA sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sclurognathi; Muroidea; Muridae; Murinae; Mus.
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mol_type="mRNA"
fsrzin=C57BL/6"
/db xref="taxon:10090"
/clone="IMAGE:5687006"
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Mus musculus
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333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdnaed/gsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
Plate: H4012 row: E column: 11
Seq primer: -21M13 Reverse
High quality sequence stop: 520
POLYA-No.
                                                                                                                                                                                                                                                                                                                                                   H4012E11-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone H4012E11 5', mRNA sequence.
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/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; This
clone is among a rearrayed set of 7,407 clones from more
CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGATATGCT 10
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VanBuren,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G.,
Martin,P.R., Stagg,C.A., Bassey,U., Aiba,K., Hamatani,T.,
Kargul,G.J., Luo,A.G., Kelso,J., Hide,W. and Ko,M.S.H.
Assembly, verification, and initial annotation of NIA 7.4K mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGCGGAGTGATGCCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Pred. No. 2.8e-06
0; Mismatches 30
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| db xref="taxon:10090"
| clone="H4012E11"
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
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/lab_host="DH10B"
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Contact: Yong Qian
Laboratory of Genetics
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/clone="INMAGE:006209"
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/dev stage="embryo 9.5 - 10.5 dpc"
/dab_host="bridged"
/dev stage="embryo 9.5 - 10.5 dpc"
/clone=lib="muhry ManAP_H00"
/clone=lib="humaP_H00"
/note="Organ: Upper Head; Vector: pXX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according Bonafo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarcs gel.First strand cDNA synthesis was primed with oligo-dr primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University lows Brain Anacomy Project (BMAP): "Gene Discovery in the poly."
                                                                                                                                                             CN527461
UI-M-HQO-cpd-e-24-0-UI.rl NIH BMAP_HQO Mus musculus cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'organism="Mus musculus"
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Location/Qualifiers
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/strain="C57BL/6"
                                                                                                                                           Mus musculus (house mouse)
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CN527461.1 GI:46855617
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

In attack of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

E (bases I to 4120)

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Radchi,J., Aizawa,K., Akimura,T., Hara,A., Hashizume,W., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,M., Hiramoto,K., Hiracka,T., Hirozane,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Satuo,R., Sakai,C., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Takaku,Y., Tanaka,T., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takada,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030422B05 product:nitric oxide synthase 3, endothelial cell, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome, Res. 10 (11), 1757-1771 (2000)
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CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
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Functional annotation of a full-length mouse cDNA collection
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/tissue type="whole brain"
/dev stage="1,5, and 15 days newborn"
/dev stage="1,5, and 15 days newborn"
/docto="brain" triple triplage resistant)"
/clone lib="NHIB MAP GVO"
/clone lib-"NHIB MAP GVO MAP
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JGI XZT65278.fwd NIH XGC tropTad5 Xenopus tropicalis cDNA clone IMAGE:7639850 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nib.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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Xenopus tropicalis
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:30620991"
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/strain="C57BL/6"
                                                      Mus musculus (house mouse)
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DLLRTELAAEVHRVLCLEQGHMFVCGDVTMATSVLQTVQRILATEGGMELDEAGDVIG
VLRDQQRYHEDIFGLTLRTQEVTSRIRTQSFSLQERQLRGAVPWSFDPPGPEIPGS"
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/bb_xref="G1:&6346807"
/translation="MGNLKSVGQEPEPPCGLGLGLGLGCGKQGPASPAPEPSQAPAP
PSPTRPAPDHSPPLTRPPDGRPFPRVKNWEVGSITYDTLSAQAQQDGPCTSRRCLGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="13 days embryo"
22. 73630
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TYQLRESELVFGAKQAWRNAPRCVGRIQWGKLQVFDARDCRTAQEMFTYICNHIKYAT
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                                                            Division of Experimental Animal Research in Riken contributed to
     Center and Genome Science Laboratory in RIKEN
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                                                                                                             prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gec.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol type="mRNA"
/dstrain=G57BL/G1"
/db_xref="FANTOM DB:6030422B05"
/db_xref="taxon:10090"
/clone="6030422B05"
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Bombyx mori cDNA
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

Xenopodinae; Xenopus; Silurana.

Richardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C., Brokatein, P. and Lindquist, E.A.

DOB Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)

Contact: Lindquist, E.A., Richardson, P.

DOB Joint Genome Institute

2800 Mitchell Drive, Walnut Creek, CA 94598, USA

Tel: 925 296 500

Fax: 925 296 500

Email: cdn@@jgi-psf.org

Tissue Procurement: Richard M. Harland Laboratory, University of
California, Berkeley; http://tropicalis.berkeley.edu/home

CDNA Library Preparation: Richard M. Harland Laboratory, University
of California, Berkeley

DNA Sequencing: DOB Joint Genome Institute: http://www.jgi.doe.gov

Clone Distribution: I.M.A.G.E. Consortium/LLNL:

http://image.llnl.gov

Naming Conventions: EST name is generated by the concatenation of
the UGI Clone Id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert.

Small Insert: Based upon one or more sequencing reads of this clone
where vector sequence was present at both ends, this clone where vector sequence as contain a cDNA insert on the order of 600-1000 bases.

High quality sequence stop: 544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NIH_XGC_tropTad5"

/note="Woetcor: pCs108; Site 1: Sal1; Site 2: Not1; Tadpole library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dT primers (Invitrogen SuperScript Plasmid System for cDNA Synthesis and Cloning). Salt [5, end) -Not1 [3, end) cDNA was inserted into vector pCs108
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/tissue_type="whole embryo"
/dev_stage="Tadpole (st. 36-41)"
/lab host="E. coli XL1-Blue derivative, Stratagene
ElecEroTen-Blue"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Murcidea; Muridae; Glires; Rodentia;
Sciurognathi; Murcidea; Muridae; Musinae; Mus.

El (bases 1 to 286)
Sciurognathi; M., Feldblyum, T., Malek, J., Shatsman, S.,
Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.,
Mouse BAC End Sequences from Library RPCI-23
Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
                                                                                                                                                                                                                                                                                                         Concome Research Group
National Institute of Agrobiological Sciences
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Tel: 81-29-838-6120
Exar: 81-29-838-6121
Email: kmita@nias.affrc.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ביימים SS 01-MAR-2000 RPCI-23-36A5.TV RPCI-23 Mus musculus genomic clone RPCI-23-36BA5, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 GGATACCAGGAGCCAGATGATGGAGATTATAGGAGATCCAGCACGAGTTGAATTTACAGAG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAACGCACCGACGGTAAACATGACTACAGAATATGGAATCCGCAGCTTATCAATTATGCA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
I (bases 1 to 721)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                         Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.7%; Score 61.2; DB 3; Length 721; 68.9%; Pred. No. 2e-05; ive 0; Mismatches 38; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Malpighian tubule"
/dev_stage="5th instar larva day 3"
/clone_lib="maV3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Bombyx mori"
Bombyx mori (domestic silkworm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="p50"
/db_xref="taxon:7091"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="maV30763"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ044226.1 GI:7138883
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BJ088070 625 bp mRNA linear EST 29-SEP-2003
BJ088070 NIBB Mochii normalized Xenopus tailbud library Xenopus
laevis cDNA clone XL091118 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            697 cháciác recertácic canda da critic cán reridán case chác recidentacides 756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
1111 Yata, Mishima, Shizuoka 411-8540, Japan
1111 Yata, Mishima, Shizuoka 411-8550, Shizuoka 411-8550, Shizuoka 411-8550, Shizuoka 411-8550, Shizuoka 411-8550, Shizuoka 411-8550, Japan
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CAGCGGAGTGATGGCAAACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="stage_25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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0
                                                                                                                                                                                                                                                                                                                                                               Score 54.8; DB 11; Length 3612; Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.1%; Score 49.4; DB 3; Length 625; 68.7%; Pred. No. 0.026; ive 0; Mismatches 31; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                'tissue_type="whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed genes in X. laevis embryo Unpublished (2001) Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Xenopus laevis"
                                                     1. .3612
/organism="Homo sapiens"
                                                                                                                     /mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL091118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 625)
                                                                                                                                                                                                                  <1. .>3612
/gene="NOS3"
/locus_tag="HC11004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://xenopus.nibb.ac.jp.
Location/Qualifiers
                          location/Qualifiers
                                                                                                                                                                                    /chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BJ088070.1 GI:17585186
                                                                                                                                                                                                                                                                                                                                                                         ch 21.2%;
1 Similarity 65.6%;
80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 19.1
Best Local Similarity 68.7
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis
alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GT 122
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 8
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BJ088070
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                              FEATURES
                                                                                                                                                                                                                                                                                                                   ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
CoRI, Site 2: BcoRI; Female C57BL/61 mouses kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
BHIOB electrocompetent cells (RRL Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 TGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae; Homo.

1 (bases 1 to 3612)

Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

A Scan for Positively Selected Genes in the Genomes of Humans and
                          Email: state of the control of the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TGGCTACCANATGCCCGATGGCACCATCAGAGGGATGCTGCCACCTTGGAGTTCACCCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Observed to 3612)

Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B. Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B. White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission

Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 200550, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DQ045247 3612 bp DNA linear GSS 02-JUI
Homo sapiens NOS3 gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.2%; Score 54.8; DB 9; Length 286; 75.2%; Pred. No. 0.00086; ive 1; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 GGTACCCGGCCCAGCCTCAGCCRCCGGCCATTGGGGCCGGGAGCC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLoS Biol. 3 (6), E170 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="RPCI-23-368A5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic survey sequence. DQ045247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                             Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15869325
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ORGANISM
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AUTHORS
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AUTHORS
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JOURNAL
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DQ045247
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KEYWORDS
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ઠે g ò 엄 ö

Sackton, T.B.,

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neoperygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

(Ypriniformes; Cyprinidae; Danio.

(Ypriniformes; Cyprinidae; Danio.

(Neses 1 to 906)

National Institutes of Health, Mammalian Gene Collection (MGC)

(Nublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Len Zon, Harvard

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGENCOURT_16541419 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7044445 CK016997
                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Pan.

(Dasses 1 to 3449)

Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubiaz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.

A Scan for Positively Selected Genes in the Genomes of Humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There is a sequence of a sequencing genomic exons and ordering the beginning of the beginning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3449;
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Pred. No. 0.16;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                      PLoS Biol. 3 (6), E170 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="NOS3"
/locus_tag="HC11004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                       troglodytes (chimpanzee)
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Danio rerio
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Best Local Similarity 65.1%;
Matches 69; Conservative (
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                                               Pan troglodytes
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CK016997
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DQ045248
DQ045248.1 GI:66896463
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Blgars 1 to 619)
Elgar, G., Clark, M.S., Smith, S., Meek, S., Warner, S., Edwards, Y.J.K.,
Umrania, Y., Williams, G. and Brenner, S.
Direct Submission
Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource
                                                                                                                                                                                                                                  GSS 25-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Generation and analysis of 25 Mb of genomic DNA from the pufferfish
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Bouchireb,N., Cottage,A., Yeo,G.S., Umrania,Y., Williams,G. and
                              343 CAAAGAACGGATATGAAGCACGACTTTAGAATCTGGAATGCTCAGCTTATTCGCTATGCT
CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                  GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Takifugu rubripes"
/mol_type="genomic DNA"
/db_xref="taxon:31033"
/clone="064007cF6"
/clone_lib="cosmid 064007"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fugu rubripes by sequence scanning
Genome Res. 9 (10), 960-971 (1999)
                                                                                                                                                                                                                                                                                             AL125658
AL125658.1 GI:6107273
GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Centre, Hinxton, Cambridge,
biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V type: phagemid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GGCTACCAGATGCCAGATGG 80
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Matches 60; Conserv
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RESULT 33 DQ045248

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Richards, S. Liu, Y., Bettencourt, B.R., Hradecky, P., Letovsky, S., Nielsen, R., Thornton, K., Hubisz, M.J., Chen, R., Meisel, R.P., Shielsen, R., Thornton, K., Hubisz, M.J., Chen, R., Meisel, R.P., Couronne, O., Hua, S., Smith, M.A., Zhang, P., Liu, J., Bussemaker, H.J., van Batenburg, M.F., Howells, S.L., Scherer, S.E., Sodergren, E., Matthews, B.B., Crosby, M.A., Schroeder, A.J., Ortiz-Barrientos, D., Wheeler, D.A., Worley, K.C., Havlak, P., Durbin, K.J., Egan, A., Gill, R., Hume, J., Morgan, M.B., Miner, G., Hamilton, C., Huang, Y., Waldron, L., Verduzco, D., Clerc-Bankenburg, K.P., Dubchak, I., Nor, M.A., Anderson, W., White, K.P., Clark, A.G., Schaeffer, S.W., Gelbart, W., Weinstock, G.M. and Gibbs, R.A.

Comparative genome sequencing of Drosophila pseudoobscura: chromosomal, gene, and cis-element evolution
                                                                                                                                   /done liber CEGERBR09"
//clone liber CEGERBR09"
//clone liber CEGERBR09"
//clone liber CEGERBR09"
Site 2: Not; This normalized library was constructed from Site 2: Not; This normalized library was constructed from site 2: Not; This normalized library was constructed from sing an oligo(dT) primer, using methylated C in the first strand strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to Not! adapters, digested with EcoR!, size-selected, and cloned into the Not! and EcoR! compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DR123141
49091370 Drosophila pseudoobscura embryonic cDNA library Drosophila
pseudoobscura cDNA clone K7 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 CCGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGGACCCTGCCAACGTGGA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CCGATATGCTGGATATCAAATGCCAGATGGGTCTGTCATAGGAGACCCTGCAAGTGTGGA 62
/tissue_type="Chondrocytes isolated from growth plate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila pseudoobscura
Drosophila pseudoobscura
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Tel: 713-798-6667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: stephenr@bcm.tmc.edu
NCB1 Trace Archive: 226697760
Insert Length: 1750 Std Brror: 0.25.
Location/Qualifiers
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Baylor College of Medicine
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Contact: Stephen Richards
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Matches 54; Conserv
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DR123141
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1 (bases 1 to 688)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

Curr. Biol. 12 (22), 1965-1969 (2002)
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603961089F1 CSEQRBN09 Gallus gallus cDNA clone ChEST936a24 5', mRNA
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University of Manchester Institute of Science and Technology
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLANLOW: Took: 1 column: 11
High quality sequence stop: 626.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.3%; Pred. No. 0.34;
Matches 65; Conservative 0; Mismatches 33; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 ATCAGAGGGACCCTGCCAACGTGGAATTCACTCAGGT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ĕ
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PO Box 88, Manchester, M60 1QD, Tel: 01612008930
Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9031"
/clone="ChEST936a24"
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BU425320.1 GI:25917996
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Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1, .688
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UI-M-HBO.cow-f-04-0-UI.rl NIH BMAP_HBO Mus musculus cDNA clone IMAGE:30648603 5', mRNA sequence. CN459880 CN459880 EST. EST.
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mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archoaauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
I (bases 1 to 797)
Abdrakhmanov, 1. 704)
Plachy, J., Korn, B. and Buerstedde, J. M.
Alarge database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function
Gallus 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 CAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGGTACCCGGCCCAG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 CCTCAGCCRCCGGCCATTGGGGCGGGGAGCCCCGTGGTGAGCGAGTGACAGAGTGGAGTTGAGCC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73
       146 TGCGAACCGGGACGCCACTCCGGAAGCCTTNNCCACCCGGNNCTGGCTCGGGGATTTGGC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438 TTCCTCGTGGGAGGAGCTTTGACCCCTCCGAGGCAGCGGCACAGCCAGACACCTGCACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Bmail: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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                                                                                                                                                                                                                                                                                                                                        AJ394075
AJ394075 dkfz426 Gallus gallus cDNA clone 17pllr1,
AJ394075
                                                                             155 GCGGGGAGCCCCCGTGGTGAGCGAGTGAGAGTGGAGCCCAGAG 198
                                                                                                                                                      43
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                                                                                                                                                      86 TCTGGGAGCCCCTTGGGGGGGGGGGGGCNNNNNNNNNNNGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Bursa of Fabricius"
/cell_type="bursal lymphocyte"
/dev_stage="2"3 weeks old"
/clone_lib="dkfz426"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66
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Pred. No. 8.9;
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/organism="Gallus gallus"
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/clone="17p11r1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="CB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGAGGAGACACGCAGCC 211
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ilarity 49.5%;
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
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                                                                                                                                                                                                                                                              /note="Vector: pOTB7; Site 1: EcoR1; Site 2: XhoI; oligo dt priming from poly A+ RNA, directionall\overline{y} cloned"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol type="mkNA"
/mol type="mkNA"
/strain="beagle"
/db xref="taxon.9615"
/lab host="EMDH10B"
/clone lib="GLGC-EMDH10B"
/iclone lib="GLGC-EMDH-CF Canis familiaris Normalized Mixed Tissue cDNA Library"
/note="Organ: heart, liver, kidney, testis, and brain; Vector: pCMVSport6.0; Site_1: Not1; Site_2: SalI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 TGGAATGCTCAGCTCATCCGCTATGCTGCTACCAGATGCCAGATGCCAGCATCAGAGGG
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                                                                                                                                              /dev_stage="0-18h embryos"
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library"
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42.4; DB 8; Length 1171; Pred. No. 1.9;
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Pred. No. 6.6;
0; Mismatches 71; Indels 4
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52.9%; Pred. No. 1.9;
-... 0; Mismatches 81; Indels
organism="Drosophila pseudoobscura"
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Tel: 301 987 1700
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                                      /mol_type="mRNA"
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/clone="K7"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DN757217.1 GI:62146330
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Canis familiaris
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1 Similarity 54.3%;
89; Conservative 0
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Gene Logic Inc.
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Beloniformes; Adrianichthyidae; Oryzias.
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//dev_stage="mille byte"
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Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAGT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
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                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha;
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                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                         1 (bases 1 to 71)
NIH-MGC http://mgr.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: pYX-5.
Location/Qualifiers
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/strain="C57BL/6"
        Mus musculus (house mouse)
Mus musculus
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Contact: Tadasu Shin-i
Contact: Sesource Information
National Institute of Genetics
1111 Yata, Mishima,
Tel: 81-559-81-6856
Fax: 81-559-81-6856
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/clone="Mrol5DA022j07"
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                                                                                                                                                                                                                                                                                                                                                             organism="Oryzias latipes"
                                                                                                                                                                                                                                                                                Email: tshini@genes.nig.ac.jp.
    Location/Qualifiers
    1. .721
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Best Local Similarity 67.9
Matches 55; Conservative
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December 13, 2005, 16:17:25 ; Search time 142 Seconds (without alignments) 3229.654 Million cell updates/sec
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9: /cgn2_6/ptodata/1/ina/RECOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1303057 segs, 888780828 residues
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 11841, A Sequence 15484, A Sequence 3742, App Sequence 11, App1 Sequence 1478, App Sequence 1, App1 Sequence 18, App1 Sequence 18, App1 Sequence 18, App1 Sequence 12, App1 Sequence 12, App1 Sequence 12, App1 Sequence 12, App1 Description Sequence Sequence Sequence US-09-949-016-155484
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25 75 29.1 4780 3 US-09-123-624-3 27 56.4 21.9 9208 3 US-08-880-342-20 29 54.8 21.2 3612 3 US-09-08-506-1 29 54.8 21.2 3610 3 US-09-08-506-1 29 54.8 21.2 3690 3 US-09-016-434-1234 31 54.8 21.2 4035 3 US-09-016-434-1369 32 51.6 20.0 4097 3 US-09-016-434-1369 33 51.6 20.0 4097 3 US-09-123-624-5 34 51.6 20.0 4097 3 US-09-123-624-5 35 51.6 20.0 4491 3 US-09-123-624-5 36 50.0 4491 3 US-09-419-171-25 37 35.4 13.7 4603 2 US-08-456-837-17 38 35.4 13.7 4603 2 US-08-456-837-17 39 35.4 13.7 4603 2 US-08-456-076A-17 39 35.4 13.7 4603 2 US-08-458-076A-17 39 35.4 13.7 4603 3 US-08-457-3214-17 39 35.4 13.7 4603 3 US-08-028-934-17 39 35.4 13.7 5698 2 US-08-729-114-17	Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 134, Ap Sequence 1369, Ap Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 25, Appli Sequence 17, Appli	
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ALIGNMENTS

Sequence 11841, Application US/09949016 Battent No. 6812339 GENERAL INFORMATION: APPLICANT: VENTER, J. Craig et al. APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLO01307 FURENT APPLICATION NUMBER: 2009-04-14 PRIOR APPLICATION NUMBER: 60/241,755 PRIOR APPLICATION NUMBER: 60/241,755 PRIOR FILING DATE: 2000-10-20 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH 47419
TYPE: DNA
ORGANISM: Human
US-09-949-016-11841

Query Match

99.8%; Score 257.6; DB 3; Length 47419;
Best Local Similarity 99.6%; Pred. No. 7e-62;
Matches 257; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Acthes 257; Conservative 0; Mismatches 0; Indels 0; Qy

21551 GTACCCGGCCCAGCCTCAGCCRCCGGCCATTGGGGCGCGGGGGGCCCCGTGGTGAGCGAGTG 180 GGCTACCAGATGCCAGATGGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120 121 61 셤 ò 요 g 원 ઠે ò

GTTCCCCAGCTGTGCATC 258

241

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us-10-713-137-1.rni

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Sequence 99, Application US/09949016

Sequence 99, Application US/09949016

Releant No. 684239

GREERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPRENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ TWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 99

LENGTH: 3855
                                                                                                                                                                                                                                                                                                                                                            999 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 1058
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                                                                                                                             Score 120.4; DB 3;
Pred. No. 5.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 120.4; DB 3;
Pred. No. 5.6e-24;
0; Mismatches 1;
                                                                                                                                                                               0; Mismatches
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Patent No. 6171856
PAPLICANT: Thigpen, Anice
APPLICANT: Hohmeier, Hans-Ewald
APPLICANT: Newgard, Christopher B.
APPLICANT: Newgard, Christopher B.
APPLICANT: Unger, Roger H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.7%;
99.2%;
                                                                                                                                46.7%;
                                                                                                                           Query Match
Best Local Similarity 99.2
Matches 121; Conservative
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Best Local Similarity 99.2
Matches 121; Conservative
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                          ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Human
     LENGTH: 3853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-949-016-99
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US-09-126-109-11
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                                                                                                           Sequence 15484, Application US/09949016

| Patent No. 6812339
| GENERAL INFORMATION |
| Patent No. 6812339
| GENERAL INFORMATION |
| TITLE OF INVENTION |
| PRIOR APPLICATION |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SEQ ID NO 15484 |
| LENGTH: 47420 |
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Patent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TUTLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PAPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PELING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PELING DATE: 2000-00-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE FASISEO for Windows Version 4.0
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99.8%; Score 257.6; DB 3; Length 47420;
Best Local Similarity 99.6%; Pred. No. 7e-62;
Matches 257; Conservative 1; Mismatches 0; Indels 0;
21552 GTTCCCCAGCTGTGCATC 21569
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US-09-949-016-15484
                                                                                                -09-949-016-15484
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61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 120
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; Sequence 1, Application US/08314917
; Patent No. 5468630
; GENERAL INFORMATION:
   APPLICANT: Billiar, Andreas K.
   APPLICANT: Simmothy R.
   APPLICANT: Geller, David A.
   APPLICANT: Simmons, Richard L.
   TITLE OF INVENTION: CDNA Clone for Human Inducible Nitric
   TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
   NUMBER OF SEQUENCES: 2
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: Arnold B. Silverman
   ADDRESSEE: Arnold B. Silverman
   ADDRESSEE: Arnold B. Silverman
   STREET: 600 Grant Street, 42nd Floor
   CITY: Pittsburgh
   STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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Pred. No. 5.7e-24;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                         ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-00:
TELECOMMUNICATION INFORMATION:
TELEFAX: (550) 845-4166
INFORMATION FOR SEQ ID NO: 1478:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.2%;
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 4062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
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US-09-016-434-1478
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Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: 1490
NUMBER OF SEQUENCES: 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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46.7%; Score 120.4; DB 3; Length 4062;
Best Local Similarity 99.2%; Pred. No. 5.7e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0;
APPLICANT: Shimabukuro, Michio
APPLICANT: Chen, Guaxun
APPLICANT: Rhodes, Christopher J.
APPLICANT: Hugl, Sigrun R.
APPLICANT: Cousin, Sharon
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO NO-MEDIATED CYTOTOXICITY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: LC-LOUS/MS-LOUS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,109
FILING DATE: 30-JUL-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,092
FILING BAPLICATION NUMBER: US 60/055,092
FILING APPLICATION NUMBER: US UNKNOWN
FILING DATE: 30-JUL-1997
RIOR APPLICATION NUMBER: US UNKNOWN
FILING DATE: 03-MAR-1998
ATTONEY/AGENT INFORMATION:
NAME: MCMIllian Nabeela R.
REGISTRATION NUMBER: V33.363
REFERENCE/DOCKET NUMBER: USD:560
TELECOMMUNICATION INFORMATION:
TELEPHOME: (512) 418-3000
TELECOMMUNICATION INFORMATION:
TELEPHOME: (512) 414-7577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERIFICS:
LENGTH: 4062 Dase Pairs
                                                                                                                                                                                                                                                                                                                                                        STREET: P.O. Box 4433
CITY: Houston
STREET Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC comp
                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 4062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 1070
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APPLICANT: David A. Geller
APPLICANT: Richard L. Simmons
TITLE OF INVENTION: Inducible Nitric Oxide Synthase
TITLE OF INVENTION: Gene for Treatment of Disease
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESSE: Lewis F. Gould, Jr.
ADDRESSEE: Lewis F. Gould, Jr.
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 1700 Market Street, Suite 3232
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECTIE TYPE: CDNA
DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
DESCRIPTION: Synthase CDNA Clone
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                    COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,046
FILING DATE: 24-JUN-1994
CLASSIFICATION: 536
ATTONREY/AGENT INPORMATION:
NAME: GOLId, Lewis F. Jr.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 119130
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION 1NPORMATION:
TELECOMMUNICATION 1NPORMATION:
TELEFRAX: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.7%; Score 120.4; DB 2;
99.2%; Pred. No. 5.7e-24;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Induced Human Hepatocyte RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 207..3668
IDENTIFICATION METHOD: Experiment
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LIBRARY: Lambda Zap II CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFOARMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 4145 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 99.23
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHROMOSOME/SEGMENT: un MAP POSITION: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNITS: unknown
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ORIGINAL SOURCE:
TISSUE TYPE: 1
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46.7%; Score 120.4; DB 2; Length 4145;
Best Local Similarity 99.2%; Pred. No. 5.7e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 15219
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Induced Human Hepatocyte RNA
                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/981,344
FILING DATE: 25-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Arnold B.
REGISTRATION NUMBER: 22,614
REFERENCE/DOCKET NUMBER: 116972
TELECOMMUNICATION INFORMATION:
TELEPHONE: (412) 566-6000
TELEPHONE: (412) 566-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 207..3668
IDENTIFICATION METHOD: Experiment
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Patent No. 5658565
GENERAL INFORMATION:
APPLICANT: Timothy R. Billiar
APPLICANT: Edith Trang
APPLICANT: Andreas K. Nussler
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (412) 566-6099
TELEX: 866172
INPORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 4145 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE: PHINOS
POSITION IN GENOME:
CHROMOSOWE/SEGMENT: unknown
MAP POSITION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
LIBRARY: Lambda Zap II CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNITS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1071 CT 1072
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                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-314-917-1
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1011 GGCTACCAGATGCCAGATGGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 1070
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                                                                                                                                                                                                      Sequence 1, Application PCTUS9311401
GENERAL INFORMATION:
APPLICANT: Billiar, Timothy R.
APPLICANT: Billiar, Andreas K.
APPLICANT: Geller, Andreas K.
APPLICANT: Simmons, Richard L.
TITLE OF INVENTION: CDNA Clone for Human Inducible Nitric
TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: PAPELICATION DATA:
APPLICATION NUMBER: PCT/US93/11401
FILING DATE: 25-NOV-1992
CLASSIFICATION NUMBER: US/07/981,344
CLASSIFICATION NUMBER: US/07/981,344
CLASSIFICATION NUMBER: 22,614
ATTORNEY/AGENT INFORMATION:
NAME: S1 Verman, Arnold B.
REGISTRATION NUMBER: 22,614
REFERENCE/DOCKET NUMBER: 22,614
FREFERENCE/DOCKET NUMBER: 116972
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR S00
TELERAX: 866172
INFORMATION FOR S00
TELERAX: 866172
INFORMATION FOR S00
TELEGRAX: 4125 566-6009
TELEGRAX: 866172
INFORMATION FOR S00
TELEGRAX: A1445 base pairs
MUMBER: LEMICTER S00
TELEGRATH: A145 base pairs
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99.2%; Pred. No. 5.7e-24;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Arnold B. Silverman
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 600 Grant Street, 42nd Floor
CITY: Pittsburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Induced Human Hepatocyte RNA
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LOCATION: 207..3668
IDENTIFICATION METHOD: Experiment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: PHINOS
POSITION IN GENOME:
CHROMOSOWE/SEGWENT: unknown
MAP POSITION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: Lambda Zap II CDNA
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Best Local Similarity 99.2
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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TISSUE TYPE:
                                                                                                   1071 CT 1072
                                                    121 GT 122
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                                                                                                   GENERAL INFORMATION:
APPLICANT: Billiar, Timothy R.
APPLICANT: Billiar, Andreas K.
APPLICANT: Obeler, Andreas K.
APPLICANT: Geller, David A.
APPLICANT: Gimmons, Richard L.
TITLE OF INVENTION: CDNA Clone for Human Inducible Nitric
TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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46.7%; Score 120.4; DB 2; Length 4145;
Best Local Similarity 99.2%; Pred. No. 5.7e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
DESCRIPTION: Synthase CDNA Clone
HVPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,522
FILING DATE:
                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lewis F. Gould, Jr.
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 1700 Market St. Suite 3232
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Induced Human Hepatocyte RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIPICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: GOULd, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 116972-6
TELECHONONICATION INFORMATION:
TELEPHONE: (215) 575-6020
TELEFAX: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 207..3668
IDENTIFICATION METHOD: Experiment
                                                      Sequence 1, Application US/08465522
Patent No. 5882908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: PHINOS
POSITION IN GENOME:
CHROMOSOME/SEGMENT: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: Lambda Zap II CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4145 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAP POSITION: UUNITS: UNKNOWN FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 207
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1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 1070
                                                                                                                                              951 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1407, Application US/09023655

Patent No. 6607899

GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart

APPLICANT: Jeffery J. Sealhamer

TITLE OF INVENTION: EXPRESSION

NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA
                                                                                                                                                                                             61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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       Length 4145;
                                                 Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 46.7%; Score 120.4; DB 3; Best Local Similarity 99.2%; Pred. No. 5.7e-24; Matches 121; Conservative 0; Mismatches 1;
Score 120.4; DB 6;
Pred. No. 5.7e-24;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION UNMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY, AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER:
TELECOMMUNICATION INFORMATION:
REFERENCE, DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 1407:
SEQUENCE CHARACTERISTICS:
  Query Match
Best Local Similarity 99.2%;
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4164 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; CLONE: 9441452
US-09-023-655-1407
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                                                                                                                                                                                                                                                                                        121 GT 122
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US-09-023-655-1407
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                             951 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
                                                                                                                        1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 1070
                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application PC/TUS9507849
GENERAL INFORMATION:
APPLICANT: University of Pittsburgh of the Commonwealth System of Higher APPLICANT: University of Pittsburgh of the Commonwealth System of Higher APPLICANT: Education
TITLE OF INVENTION: Inducible Nitric Oxide Synthase
TITLE OF INVENTION: Gene for Treatment of Disease
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lewis F. Gould, Jr.
ADDRESSEE: Lewis F. Gould, Jr.
ADDRESSEE: Lewis F. Gould, Jr.
STREET: 1700 Market Street, Suite 3232
                                                                                                61 GGCTACCAGATGCCAGATGACATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4145 base pairs
TYPE: nucleic acid
STRANDEDNES: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
DESCRIPTION: Synthase CDNA Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE TYPE: Induced Human Hepatocyte RNA INMEDIATE SOURCE:
LIBRARY: Lambda Zap II CDNA CLONE: PHINOS POSITION IN GENOME:
CHROMOSOME/SEGMENT: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOULD, Lewis F. Jr.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 119130-2
TELECHONE: (215) 575-6020
TELEPAX: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 207..3668
LDENTIFICATION METHOD: Experiment
PCT-US95-07849-1
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PCT-US95-07849-1
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                                 1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4110;
                                                                                                                                                                                                                                                                                                                                                                                                                35.5%; Score 91.6; DB 3; Length 41
84.4%; Pred. No. 5.8e-16;
tive 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 91.6; DB 3; Length 4:
Pred. No. 5.8e-16;
0; Mismatches 19; Indels
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Best Local Similarity 84.4
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 84.4'
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus US-09-123-624-1
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SEQ ID NO 1
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                                                                  1089
970 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1029
                               61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                      1030 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTAG
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                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Xie, Qiao-wen
APPLICANT: Nathan, Carl F.
APPLICANT: Nathan, Carl A.
APPLICANT: Mumford, Richard A.
APPLICANT: Calaycay, Jimmy Ramos
TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase
TITLE OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
CITY: Rahway
STATE: New Jersey
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Pred. No. 5.7e-16;
0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: Macintosh Centris650

OPERATING SYSTEM: Macintosh 7.0.1

SOFTWARE: Microsoft Word 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/147,812

FILING DATE: No. 5766909 Available

CLASSIPICATION 1435

PRIOR APPLICATION 1435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/841,641

PILING DATE: 02-FBB-1992

ATTORNEY/AGENT INFORMATION:

NAME: Wallen, John W III

REGISTRATION NUMBER: 35,403

REFECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                      Sequence 4, Application US/08147812
Patent No. 5766909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 84.4%;
Matches 103; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 138825
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4041 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOPOLOGY: linear
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                                                                                                                                     1090 CT 1091
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                                                                                                                                                                                        RESULT 13
US-08-147-812-4
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Gaps

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION UNDRER: 37,071
REFERENCE/DOCKET UNDRER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1477:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4079 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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US-09-016-434-1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1532 ATA 1534
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LIBRARY: GENB
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                                        978 GGCTACCAGATGCCCCGATGGCACCATCAGAGGGGATGCTGCCACCTTGGAGTTCACCCAG 1037
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61 GGCTACCAGATGCCAGATGGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08147812
Patent No. 576509
GENERAL INFORMATION:
APPLICANT: Xie, Qiao-wen
APPLICANT: Nathan, Carl F.
APPLICANT: Munford, Richard A.
APPLICANT: Munford, Jümmy Ramos
TITLE OF INVENTION: DA Encoding Inducible Nitric Oxide Synthase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEB: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 5.8e-16;
0; Mismatches 19; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macincoh Centrise50
OPERATING SYSTEM: Macincoh Centrise50
OPERATING SYSTEM: Macincoh 7.0.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,812
FILING DATE: No. 5766909 Available
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/14,641
APPLICATION NUMBER: 07/841,641
ATTORNEY AGENT INFORMATION:
NAME: WALLE, JOHN W III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 186581A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 84.4%;
Matches 103; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (908) 594-3905
(908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (908) 594-4720
TELEX: 138825
INPORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 4165 bases
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New Jersey
COUNTRY: USA
ZIP: 07065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-08-147-812-6
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US-08-147-812-6
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61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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US-09-016-434-1477

Sequence 1477, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OP SEQUENCES: 1499
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: ALO ALLO
CITY: PALO ALLO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Patent No. 5834306
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Namette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFTCATION:
PARCE APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 30.3%; Score 78.2; DB 3; 18est Local Similarity 77.2%; Pred. No. 3e-12; Matches 95; Conservative 0; Mismatches 28;
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ADDRESSEE: Dehlinger & Associates
              STREET: 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MYDGECULE TYPE: CDNA to mRNA
HYPOTHETICLE NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al,
INDIVIDUAL ISOLATE: J. Neurochem 63:140 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Mirphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/365,486A

FILING DATE: 23-DEC-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615

REGISTRATION NUMBER: 38,615

RELEFENCE/POCKET NUMBER: 38,615

TELECOMMUNICATION INFORMATION:

TELEFONE: (415) 324-0860

TELEFAN: (415) 324-0860

TELEFAN: (415) 324-0960

TRELEFAN: (415) 324-0960

TRELEFAN: (415) 324-0960

TRELEFAN: (415) 324-0960

TRELEFAN: (415) 324-0960
         Therapeutic Constructs
                          STREET: 350 Cambridge & Associates STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto COINVIII. CA COINVIII.
                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6218179
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4353 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                            ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
  TITLE OF INVENTION: Th
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 1..4305
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                                                                                                                                                                 USA
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                                                                                                                                                                 COUNTRY:
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61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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Pred. No. 3.1e-12;
0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human NOS-1 gene, Fujisawa, et al,
J. Neurochem 63:140 1994
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US-08-365-46A-12
Sequence 12, Application US/08365486A
Sequence 12, Application US/08365486A
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                      CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 23-JUN-1997

CLASSIFICATION TO 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IB95/00996

FILING DATE: 13-NOV-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/365,486

FILING DATE: 23-DEC-1994

ATTORNEY/AGENT INFORMATION:
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8255-0018.30
                                                                               ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 4353 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 77.2%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..4305
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1738 cagadgacrgacggcaacargacrrccgagrgrggaacrcgcagcrcarccgcracgcg 1797
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Batent No. 5268465

GENERAL INFORMATION:
APPLICANT: Bredt, David S.
APPLICANT: Hwang, Paul M.
APPLICANT: Sredt, Randall
APPLICANT: Snyder, Solomn H.
TITLE OF INVENTION: Purification and Molecular Cloning of Nitric
TITLE OF INVENTION: Oxide Synthase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSES: Banner, Birch, McKie & Beckett
STREET: One Thomas Circle, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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                                                                                                                                                                                         CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/880,342

FILING DATE: 23-JUN-1997

CLASSIPICATION: 514

PRIOR APPLICATION NUMBER: US/08/880,342

FILING DATE: 13-NOV-1995

PROR APPLICATION NUMBER: US/08/365,486

FILING DATE: 13-NOV-1995

PROR APPLICATION NUMBER: US/08/365,486

FILING DATE: 23-DEC-1994

ATTONNEY/AGENT INPORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615

REGISTRATION NUMBER: 38,615

REGISTRATION NUMBER: 38,615

TELEPHONE: (415) 324-0980

TELEPHONE: (415) 324-0980

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LEMOTH: 5057 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rat bNOS cDNA
                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.3%;
Best Local Similarity 76.2%;
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-880-342-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-880-342-12

Sequence 12, Application US/0880342

Sequence 12, Application US/0880342

Patent No. 6218179

GENERAL INFORMATION:

APPLICANT: Webster, Keith A.

APPLICANT: Marchy, Brian

APPLICANT: Laderoute, Keith R.

APPLICANT: Laderoute, Keith R.

APPLICANT: Laderoute, Seith R.

APPLICANT: Applicant Green, Christopher J.

TITLE OF INVENTION: Tissue Specific Hypoxia Regulated

TITLE OF INVENTION: Therapeutic Constructs

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: ADDRESSEE:

ADDRESSEE: ADDRESSEE:

ATREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                        COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTONEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 925-0018
TELEPHONE: (415) 324-0880
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5057 base pairs
"TUBOR TELEPHONE OF THE OPERATION OPERAT
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE: rat bNOS cDNA
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Best Local Similarity 76.2
Matches 93; Conservative
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STRANDEDNESS: double
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LOCATION: 349..4638
                        STREET: 350
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US-09-123-708-3

Sequence 3, Application US/09123708

Sequence 3, Application US/09123708

SENERAL INCPRARATION:

APPLICANT: SCHRADER, Juergen

TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS

TITLE OF INVENTION: TREATMENT US/09/123,708

CURRENT APPLICATION NUMBER: US/09/123,708

CURRENT FILING DATE: 1998-07-28

EARLIER APPLICATION NUMBER: 08/553,503

BARLIER APPLICATION NUMBER: 08/553,503

BARLIER PILING DATE: 1994-03-31

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PAGENTIN VOICE: 20

SEQ ID NO 3

LENGTH: 4780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGAGAATGCTCAGCTCATCCGCTATGCT
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75.6%; Pred. No. 2.4e-11;
tive 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human NOS-SN gene, Nakane, et al, FEBS Lett 316:175 (1993)
CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/365,486A

FILING DATE: 23-DEC-1994

CLASSIFICATION: 514

ATTONNEY/AGENT INPORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615

REFRENCE/DOCKET NUMBER: 9255-0018

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF 24-0960

INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHRARACTERISTICS:

LENGTH: 4790 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                LENGTH: 4780 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.69
Warrhes 93; Conservative
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; ORGANISM: Cytomegalovirus
US-09-123-708-3
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TOCATION: 431..4732
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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Pred. No. 1.7e-11;
0; Mismatches 29; Indels 0
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; Sequence 20, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
    APPLICANT: Webster, Keith A.
    APPLICANT: Bishopric, Nanette H.
    TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
    TITLE OF INVENTION: Therapeutic Constructs
    TITLE OF SEQUENCES: 31
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Dehlinger & Associates
    STREET: 350 Cambridge Avenue, Suite 250
    CITY: Palo Alto
    STATE: CA
    COUNTRY: USA
                                                COMPUTER: Eloppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,002
FILING DATE: 19910118
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: Kagan, SATEA A.
NAMME: Kagan, SATEA A.
REGISTRATION NUMBER: 1107.033576
TELEPOMOUNICATION INFORMATION:
TELEPOMOUSE: (202) 296-5500
TELEPAN: (202) 296-5500
TELEPAN: (202) 296-5500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5108 base pairs
TYPE: NUCLEIC ACID
STRANDEDINESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ORGANISM: Rattus rattus
TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.37
Best Local Similarity 76.29
Matches 93; Conservative
                    ZIP: 20005
COMPUTER READABLE FORM:
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OTHER INFORMATION:
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MOLECULE TYPE: CI
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LOCATION: 400
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ANTI-SENSE: N
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Palo Alto
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US-08-880-342-20
                                                 COUNTRY:
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Sequence 3, Application US/09123624

Patent No. 614936

GENERAL INPORMATION:

APPLICANT: GCHRADER, Jurgen

TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS

FILE REPERROR: 511169-2004

CURRENT APPLICATION NUMBER: US/09/123,624

CURRENT FILING DATE: 1998-07-28

PRIOR FILING DATE: 1996-03-01

PRIOR FILING DATE: 1996-03-01

PRIOR FILING DATE: 1994-03-31

NUMBER OF SEQ ID NOS: 6

SOFTWARE PATENTIN Ver: 2.1

SEQ ID NO 3

LENGTH 4780
                                                                                         1832 CAGAGGACAGACGACAGCACGACTICCGAGTCTGGAACTCCCAGCTCATGCTACGCT 1891
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                                                              1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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APPLICANT: Webster, Keith A.
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRIBESS:
STREET: 350 Cambridge Avenue, Suite 250
75.6%; Pred. No. 2.4e-11; indels ive 0; Mismatches 30; Indels
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75.6%; Pred. No. 2.4e-11;
tive 0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/08880342
Patent No. 6218179
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Best Local Similarity 75.6
Matches 93; Conservative
                      93; Conservative
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ORGANISM: Homo sapiens
Best Local Similarity
Matches 93; Conserva
                                                                                                                                                                                                                                                                               1952 ATA 1954
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1832 CAGAGGACAGACGGCAAGCACGACTTCCGAGTCTGGAACTCCCAGCTCATCCGCTACGCT 1891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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Batent No. 6569618
GENERAL INFORMATION:
APPLICANT: YASUE, Hirofumi
APPLICANT: YOSHIWURA, Kumamoto
TITLE OF INVENTION: DIAGNOSIS OF DISEASES ASSOCIATED WITH CORONARY
TITLE OF INVENTION: TWITCHING
FILE REFERENCE: 0032-245P
CURRENT FILLING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 29.1%; Score 75; DB 3; Length 4780; Best Local Similarity 75.6%; Pred. No. 2.4e-11; Matches 93; Conservative 0; Mismatches 30; Indels
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                                                                                                                                                                                                       MEDIUM TYPE: FLODPY G18K

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/880,342

FILING DATE: 23-JUN-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IB95/00996

FILING DATE: 13-NOV-1995

PRIOR APPLICATION NUMBER: US 08/365,486

FILING DATA:

APPLICATION NUMBER: US 08/365,486

FILING DATE: 23-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REFERENCZ/DOCKET NUMBER: 38,615

REFERENCZ/DOCKET NUMBER: 38,615

REFERENCZ/DOCKET NUMBER: 324-0860

TELEPHONE: (415) 324-0860

TELEPHONE: (415) 324-0960

INFORMATION FOR SEQ ID NO: 20:
SEQUIRNEE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                   COMPUTER READABLE FORM:
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USA
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CORRESPONDENCE ADDRESS:
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Patent No. 6569618
GENERAL INFORMATION:
APPLICANT: YASUE, Hirofumi
APPLICANT: YOSHIMURA, Kumamoto
TITLE OF INVENTION: DIAGNOSIS OF DISEASES ASSOCIATED WITH CORONARY
TITLE OF INVENTION: TWITCHING
FILE REFERENCE: 0032-245P
CURRENT APPLICATION NUMBER: US/09/068,506A
CURRENT FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jaffee Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
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                                                                                                          PEATURE:
OTHER INFORMATION: nnnnnnnnn = Intervening sequences of introns
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                                                                                                                                                                                          21.9%; Score 56.4; DB 3; Length 9208; 66.4%; Pred. No. 4.1e-06;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1234, Application US/09016434
Patent No. 650038
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.0
      SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                Best Local Similarity 66.4
Matches 81; Conservative
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US-09-068-506-2
                                                                    TYPE: DNA ORGANISM: Homo sapiens
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Matches 80; Conserv
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LENGTH: 3612
                          SEQ ID NO 1
LENGTH: 9208
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US-09-068-506-2
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61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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US-009-016-434-1369
US-009-016-434-1369
Sequence 1369, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Jaffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS: 1490
CORRESPONDENCE ADDRESS: BHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54.8; DB 3;
Pred. No. 9.5e-06;
0; Mismatches 42;
PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INPORMATION FOR SEQ ID NO: 1234:
SEQUENCE CHARACTERISTICS:
  ADDRESSEE: INCYTE PHARMACE
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 21.2%;
Best Local Similarity 65.6%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3690 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                              HEREWITH
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CALIFORNIA
                                  PALO ALTO
CALIFORNIA
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; CLONE: 9189259
US-09-016-434-1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic
STRANDEDNESS:
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                                                                                                                                                                                                                                                FILING DATE:
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ZIP: 94304
                                                                                            ZIP: 94304
                                                          STATE: CA
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61 GCCTACCAGATGCCAGATGCCAGACCATCAGAGGGGACCCTGCCAACGTGGAATTCACTTCAG 120
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FILE REFERENCE: 511169-2003
CURRENT PELLOR NUMBER: US/09/123,708
CURRENT FILING DATE: 1998-07-28
EARLIER APPLICATION NUMBER: 08/553,503
EARLIER FILING DATE: 1996-03-01
EARLIER FILING DATE: 1996-03-01
EARLIER FILING DATE: 1994-03-31
NUMBER: OF SEQ ID NOS: 6
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                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,912
FILING DATE: 17-UL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Milonig, Robert C.
REGISTRATION NUMBER: 069.4280001/JAG/RCM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 51.540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09123708 Patent No. 6146887
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Axel
                                 17-JUL-1997
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US-09-123-708-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-08-896-053-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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APPLICANT: SCHRADER,
APPLICANT: GOEDECKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GT 122
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LENGTH: 4097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-123-708-5
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Patent No. 6720309
GENERAL INFORMATION:
APPLICANT: Janssens, Stefans
APPLICANT: Bloch, Kenneth D.
APPLICANT: Collen, D sir
TITLE OF INVENTION: Method of Inducing Vasodilation and
TITLE OF INVENTION: Transfer of the Nitric Oxide Synthase Gene
TITLE OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        748 cadcicercicecricices as a contración a construcción de constructos de contraciones de contración de contración
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
PLING DATE: HEREWITH
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIPICATION:
ATTOMNEN FROM INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1369:
SEQUENCE CHARACTERISTICS:
LENGTH: 4035 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Sterne, Kessler, Goldstein & Fox P.L.L.C. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,053
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; CLONE: 9434699
US-09-016-434-1369
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IMMEDIATE SOURCE
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1440 GT 1441
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SEQ ID NO 25
LENGTH: 4491
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US-09-419-371-25
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                                                                                                                     US-09-123-624-5

US-09-123-624-5

Sequence 5, Application US/09123624

Patent No. 614996

GENERAL INFORMATION:

APPLICANT: SCHRADER, Jurgen

APPLICANT: SCHRADER, Jurgen

APPLICANT: GODGCKE, Axel

TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS

FILE REPRESENCE: 511169-2004

CURRENT APPLICATION NUMBER: US/09/123,624

CURRENT APPLICATION NUMBER: 08/553,503

PRIOR APPLICATION NUMBER: 4411402.8

PRIOR PILING DATE: 1994-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
20.0%; Score 51.6; DB 3; Length 4097;
Best Local Similarity 62.3%; Pred. No. 7.5e-05;
Matches 81; Conservative 0; Mismatches 49; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02173

ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy Size
COMPUTER: Floppy Size
COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Application US/08809917
Patent No. 6689557
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
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121 GTACCCGGCC 130
                                     вво стстесатсс ввэ
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US-09-123-624-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 5
LENGTH: 4097
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GENERAL INFORMATION:
APPLICANT: Tully, Timothy P.
APPLICANT: Tully, Timothy P.
TITLE OF INVENTION: Cloning and Characterizing of Genes;
TITLE OF INVENTION: Associated With Long-Term Memory;
TITLE OF INVENTION: Associated With Long-Term Memory;
FILE REFERENCE: CSHL94-03A3Z;
CURRENT FILING DATE: 1999-10-14;
PRIOR FILING DATE: 1999-10-17;
PRIOR FILING DATE: 1995-10-07;
PRIOR FILING DATE: 1995-10-06;
PRIOR FILING DATE: 1994-12-21;
PRIOR FILING DATE: 1994-12-21;
PRIOR FILING DATE: 1994-12-21;
PRIOR FILING DATE: 1994-10-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Indels
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Pred. No. 7.6e-05;
0; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 20.0%; Score 51.6; DB 3; Best Local Similarity 63.9%; Pred. No. 7.6e-05; Matches 78; Conservative 0; Mismatches 44;
                                                                                                                                                                                                      NAME: Grandhan, Patricia
REGISTRATION NUMBER: 32.227
REFERENCE/DOCKET NUMBER: CSHL94-03A2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-9540
INFORMATION FOR SEQ ID NO: 25:
APPLICATION NUMBER: PCT/US95/13198 FILING DATE: APPLICATION NUMBER: US 08/361,063 FILING DATE: 21-DEC-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/319,866 FILING DATE: 07-OCT-1994 ATTORNEY/AGENT INFORMATION: NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 25, Application US/09419371
; Patent No. 6890516
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Best Local Similarity 63.9%;
Matches 78; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 4491 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-809-917-25
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LOCATION: 1598..2758
OTHER INFORMATION: /gene= "phz2"
OTHER INFORMATION: /label= ORF2
OTHER INFORMATION: /note= "Open Reading Frame #2 for DNA sequence"
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OTHER INFORMATION: /label= ORF1
OTHER INFORMATION: /note= "Open Reading Frame #1 for DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAPPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC Compatible
OPERATING SYSTEM: PC-0DS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,261B
FILING DATE: 08-JUN-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFRENCE/DOCKET NUMBER: 36,129
REFRENCE/COMMUTION: INFORMATION:
TELEPHONE: 919-541.8614
                                                                                                                                                                                                                                                                 APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Hill, Dwight Steven
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Ciba-Geigy Corporation
7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 2764..3597
OTHER INFORMATION: /gene= "phz3"
OTHER INFORMATION: /label= ORF3
                                                                                                                                                                            US-08-258-261B-17/c
; Sequence 17, Application US/08258261B
; Patent No. 5639949
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4603 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                          121 GTACCCGGCC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1598..2758
                                                                          852 CTCTGCATCC 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 230..1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 7 SKy...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                       RESULT 37
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                          ò
                                             1320 caacgcacagargccaagcargarrarcgcarrrggaaraaccaarraararcrrargcc 1379
                                                                                                                                               1380 decracadecadecedardeaaaarcarredecearcecareaareredacriracada 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                  61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GECTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     732 chácicececedádececegadherrecidareradahengechádradradechacinada
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1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Harrison, David G.
APPLICANT: Alexander, R. Wayne
APPLICANT: Murphy, T.J.
APPLICANT: Murphy, T.J.
APPLICANT: Mishida, Ken'ichi
TITLE OF INVENTION: Endothelial Nitric Oxide Synthase
TITLE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30109-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: ROPE COMPATIBLE
OPERATING SYSTEM: PC-COMPATIBLE
OPERATING SYSTEM: PC-COMPATIBLE
OPERATING SYSTEM: PC-COMPATIBLE
OPERATING SYSTEM: DG-COMPATIBLE
STILING DATE: 19920702
CLASSIPICATION: 435
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: EWU 111
REGISTRATION NUMBER: EWU 111
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
TUNFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Kilpatrick & Cody
1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                    US-07-908-245-1; Sequence 1, Application US/07908245; Patent No. 5498539; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4089 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
ORGANISM: Bovine
TISSUE TYPE: Aorta
CELL TYPE: Endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: lines MOLECULE TYPE: CI HYPOTHETICAL: NO
                                                                                                                                                                                                                                                 1440 GT 1441
                                                                                                                                                                                                    121 GT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-908-245-1
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/note= "Open Reading Frame #4 of DNA sequence. This informaris repeated in SEQ ID NO:21 due to overlapping ORFs."
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                                                                                                                                                                                                                                                                                                                                         LOCATION: 230..1594
OTHER INFORMATION: /gene= "phz1"
OTHER INFORMATION: /label= ORF1
OTHER INFORMATION: /note= "Open Reading Frame #1 for DNA sequence"
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OTHER INFORMATION: /label= ORF3
OTHER INFORMATION: /label= ORF3
OTHER INFORMATION: /note= "Open Reading Frame #3 for DNA sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3597.4262
OTHER INFORMATION: /label= ORF4
OTHER INFORMATION: /label= ORF4
OTHER INFORMATION: /sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1598..2758
OTHER INFORMATION: //gene= "phz2"
OTHER INFORMATION: //label= ORF2
OTHER INFORMATION: //note= "Open Reading Frame #2 for DNA sequence"
FEATURE:
NAME/KEY: CDS
LOCATION: 2764..3597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.7%; Score 35.4; DB 2; Length 4603; Best Local Similarity 57.8%; Pred. No. 2.4; Matches 63; Conservative 0; Mismatches 46; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 GGCGACCTGATGCAGGCCGCCGTCGGAAGCGCACTCGCTGACGTCG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1.4603
OTHER INFORMATION: /note= "Four open reading frames OTHER INFORMATION: Example 18 of the specification."
US-08-456-837-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ligon, James M.
APPLICANT: Bigon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the syn
TITLE OF INVENTION: antipathogenic su
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ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 17, Application US/08457342; Patent No. 5662898
                                SEQUENCE CHARACTERISTICS:
LENGTH: 4603 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schupp, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Schupp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Hawthorne
                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 39
US-08-457-342-17/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FATURE
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                            FEATURE:
NAME/KEY: misc_feature
LOCATION: 3597...4262
OTHER INFORMATION: /note= "Open Reading Frame #4 of DNA sequence. This informat OTHER INFORMATION: | /note= "Open Reading Frame #4 of DNA sequence. This informat OTHER INFORMATION: | /note= "Open Reading Frame #4 of DNA sequence. This informat OTHER INFORMATION: | /note= "Open Reading Frame #4 of DNA sequence. This informat CATHER INFORMATION: | /note= "Four open reading frames |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 caccecacinariescrusceaesesrucaescecececececacaescerrus 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAGCGGAGTGATGCCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
    OTHER INFORMATION: /note= "Open Reading Frame #3 for DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 egcgaccrgargecaggccggcggcarccgaagcgcacrcgcrgacgrcg 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.7%; Score 35.4; DB 2; Length 4603; Best Local Similarity 57.8%; Pred. No. 2.4; Matches 63; Conservative 0; Mismatches 46; Indels 0
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/456,837

FILING DATE: 01-JUN-1995

PRIOR APPLICATION NUMBER: 08/457,205

FILING DATE: 01-JUN-1995

APPLICATION NUMBER: 08/457,205

FILING DATE: 01-JUN-1995

APPLICATION NUMBER: 08/457,205

FILING DATE: 08-JUN-1994

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schupp, Thomas
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Ciba-Geigy Corporation
7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/08456837
Patent No. 5643774
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CITY: Hawthorne
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Schupp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10532
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//gene= "phz3"
/label= ORF3
/note= "Open Reading Frame #3 for DNA sequence"
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/label= ORF1
/note= "Open Reading Frame #1 for DNA sequence"
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/label= ORF2
/note= "Open Reading Frame #2 for DNA sequence"
109 GGCGACCTGATGCAGGCCGGCGCATCGGAAGCGCACTCGCTGACGTCG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,646A
FILING DATE: 01-JUN-1995
CLASSIFICATION: 530
RIOR APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
ATTORNEY AGENT INFORMATION:
REFERENCE OB-JUN-1994
ATTORNEY AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: GC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 17:
SEQUIRACE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 17:
SEQUIRACE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                         APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip B.
APPLICANT: Hammer, Phillip B.
APPLICANT: Uknes, Scott Joseph
                                                                                                                          Sequence 17, Application US/08457646A Patent No. S679560 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                         APPLICANT: Schupp, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4603 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEATURE:
NAME/KEY: CDS
LOCATION: 2764..3597
OTHER INFORMATION: /Je
OTHER INFORMATION: /Ino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 230..1594
OTHER INFORMATION: /g
OTHER INFORMATION: /r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10532
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1598..2758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1598..2756
OTHER INFORMATION: ,
OTHER INFORMATION: ,
OTHER INFORMATION: ,
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                                                                            RESULT 40
US-08-457-646A-17/c
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NAME/KEX: misc_feature
LOCATION: 3597..4262
OTHER INFORMATION: /label= ORF4
OTHER INFORMATION: /note= "Open Reading Frame #4 of DNA sequence. This OTHER INFORMATION: is repeated in SEQ ID NO:21 due to overlapping ORFs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 caccecaéraarederreceaegerrecaededededegeredeaegerrrreraeceder 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: CDS
LOCATION: 1598..2758
OTHER INFORMATION: /gene= "phz2"
OTHER INFORMATION: /label= ORF2
OTHER INFORMATION: /note= "Open Reading Frame #2 for DNA sequence"
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 230..1594
OTHER INFORMATION: /Gene= "phz1"
OTHER INFORMATION: /Label= ORF1
OTHER INFORMATION: /Label= ORF1
OTHER INFORMATION: /note= "Open Reading Frame #1 for DNA sequence"
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OTHER INFORMATION: /gene= "phz3"
OTHER INFORMATION: /label= ORF3
OTHER INFORMATION: /noce= "Open Reading Frame #3 for DNA sequence"
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LOCATION: 1..4603
OTHER INFORMATION: /note= "Four open reading frames
OTHER INFORMATION:
OTHER INFORMATION: Example 18 of the specification."
                                                                                                                                                                   OPERATION SYSTEM:

OPERATION OF PATENTING SYSTEM:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/457,342

FILING DATE: U-JUN-1995

CLASSIPICATION: 424

PR.OR APPLICATION NUMBER: US/08/457,205

FILING DATE: 01-JUN-1995

APPLICATION NUMBER: 08/258,261

FILING DATE: 01-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Elmer, James Scott

REGISTRATION NUMBER: 36,129

REFERENCE/DOCKET NUMBER: CGC 1506/CIP3

TELEDHOME: 919-541-8614

TELEPHOME: 919-541-8614

TELEPHOME: 919-541-8614

TELEPHOME: 919-541-8619

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 4603 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOUS: TIMER

TOPOLOUS: TIMER

TOPOLOUS: TIMER

TOPOLOUS: Jinear

MOLECULE TYPE: DNA (Genomic)
                     COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MAMB/KEY: misc_feature

LOCATION: 3597..4262

LOCATION: 3597..4262

OTHER INFORMATION: /label= ORF4

OTHER INFORMATION: is repeated in SEQ ID NO:21 due to overlapping ORFs."

FRATURE:
NAME/KEY: misc_feature

LOCATION: 1..4603

OTHER INFORMATION: /note= "Four open reading frames

OTHER INFORMATION: /note= "Four open reading frames

OTHER INFORMATION: Example 18 of the specification."
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                                                                                                                                                                                                                                                                                                                     Query Match
13.7%; Score 35.4; DB 2; Length 4603;
Best Local Similarity 57.8%; Pred. No. 2.4;
Matches 63; Conservative 0; Mismatches 46; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 GGCGACCTGATGCAGCCGGCGCCATCGGAAGCGCACTCGCTGACGTCG 61
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sequence 621, App
Sequence 3, Appl
Sequence 10, Appl
Sequence 14, Sequence 14, Appl
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Sequence 5684, Ap
Sequence 19182, A
Sequence 19182, A
Sequence 51193, A
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Sequence 51193, A
Sequence 51194, A
Sequence 19177, A
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2680.276 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-10-741-601-5684

US-10-741-601-19182

US-10-741-600-17734

US-10-741-600-51219

US-10-741-600-51193

US-10-741-600-51193

US-10-741-600-51193

US-10-741-600-51214

US-10-741-601-19177

US-10-220-282A-1

US-10-220-282A-1

US-10-230-282A-1

US-10-230-282A-1

US-10-230-282A-1

US-10-230-282A-1

US-10-247-82A-1

US-10-247-82A-1

US-10-247-82A-1

US-10-147-82A-1

US-10-147-82A-1

US-10-147-82A-1

US-10-741-601-228

US-10-741-601-228
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US-10-741-600-622
US-10-688-845-37
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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258
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Sequence 123, App
Sequence 119, App
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Sequence 100, App
Sequence 106, App
Sequence 1177, Ap
Sequence 1477, Ap
Sequence 1, Appl
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Sequence 134, Ap
Sequence 134, Ap
Sequence 114, App
Sequence 144, App
Sequence 144, App
Sequence 5, Appli
Sequence 5, Appli
Sequence 140, App
Sequence 5, Appli
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US-10-929-182-33
US-09-870-759-123
US-09-751-708A-123
US-10-428-817A-119
US-10-377-758A-100
US-10-377-758A-100
US-10-31-467-966
US-10-631-467-966
US-10-631-467-966
US-10-305-720-1477
US-10-305-720-1477
US-10-899-121-8
US-10-305-720-1369
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US-11-097-143-14651
US-10-278-698-165
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ALIGNMENTS

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61 GCTACCAGATGCCAGATGGCAGCATCAGAGGGACCCTGCCAACGTGGAATTCACTCAG 120
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NESOLE 1.

VE-10-713-137-1

Sequence 1, Application US/10713137

Sequence 1, Application US/2050106573A1

Sequence 1, Application No. 1220650106573A1

GENERAL INFORMATION:

APPLICANT: Pasha, Abdul Qadar Mohammad

APPLICANT: Ahsan, Aarif

TITLE OF INVENTION: A method of detection of predisposition

TITLE OF INVENTION: A co high altitude pulmonary edema (HAPE)

FILE REFERENCE: 09755-0018US1

CURRENT PAPLICATION NUMBER: US/10/713,137

CURRENT FILING DATE: 2003-11-13

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-70;
Matches 258; Conservative 0; Mismatches 0; Indels 0
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US-10-713-137-1
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Sequence 51219, Application US/10741600
| Publication No. US20050026169A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: CARGILL, Michele et al.
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
| TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
| CURRENT APPLICATION NUMBER: US/10/741,600
| CURRENT PILING DATE: 2003-12-22
| NUMBER OF SEQ ID NOS: 73997
| SEQ ID NO 51219
| LENGTH: 201
                                                            25433 GTACCCGGCCCAGCCTCAGCCRCYGGCCATTGGGGCGGGGAGCCCCRTGGTGAGCGAGTG 25492
                                                                                                                                                            25493 ACAGAGTGAGCCCAGAGAGAGACACGCAGCCCGGGCTTACAGACTCACAGGCCCCGTCTT 25552
                                 61 CAACGTGGAATTCACTCAGGTACCCGGCCCAGCCTCAGCCRCCGGCCATTGGGGGCGGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GCCCCTGGTGAGCGAGTGACAGAGTGGGAGCCCAGAGGAGAGACACGCAGCCCGGGCTTACA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 GCCCCGTGGTGAGGGAGTGACAGAGTGGAGCCCCAGAGGAGACACGCAGCCCGGGCTTACA 221
                                                                                                                                                                                                                                                                                                                                 RESULT 4

US-10-741-601-19182

US-20-741-601-19182

Sequence 19182, Application US/10741601

Publication No. US20040166519A1

GENERAL INFORMATION:

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01500

CURRENT APPLICATION NUMBER: US/10/741,601

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SOFTWARE: FastSEQ for Windows Version 4.0

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LEMOTH: 201
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                                                                                                                                     181 ACAGAGTGGAGCCCAGAGGAGACACGCAGCCCGGGCTTACAGACTCACAGGCCCGTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 GACTCACAGGGCCCGTCTTGT 242
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US-10-741-601-19182
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; ORGANISM: Homo sapiens
US-10-741-600-51219
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US-10-741-600-51219
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Publication No. US20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE REFERENCE: CLO01499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 17734
LENGTH: 55689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25313 CAGCGGAGTGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 25372
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US-10-741-601-5684

Sequence 5684, Application US/10741601

Sequence 5684, Application US/10741601

Publication No. US2040166519A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL001500

CURRENT APPLICATION NUMBER: US/10/741,601

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SOFTHARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 256.8; DB 7; Length 55689;
Pred. No. 2.3e-70;
2; Mismatches 0; Indels 0;
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Best Local Similarity 99.27
Matches 256; Conservative
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) ORGANISM: Homo sapiens
US-10-741-601-5684
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-741-600-17734
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LENGTH: 55689
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; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 51193 ; LENGTH: 201
                                                                                                                        Query Match
Best Local Similarity 99.0'
Matches 199; Conservative
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US-10-741-601-19177
                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-10-741-600-51193
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US-10-741-600-51214
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Sequence 51193, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:

TITLE OF INVENTION: GENERAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997
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                                                                                                                                            CAACGTGGAATTCACTCAGGTACCCGGCCCCAGCCTCAGCCRCCGGCCATTGGGGCGGGA 161
                                                                                                                                                                GCCCCGTGGTGAGCGAGTGACAGAGTGGAGCCCAGAGGAGACACGCAGCCCGGGCTTACA 221
                                                                         42 TCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGC 101
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| Sequence 19156, Application US/10741601
| Sequence 19156, Application US/10741601
| Publication No. US20040166519A1
| GENERAL INPORMATION:
| APPLICANT: CARCILL, Michele et al.
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
| TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: GENOSIS, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: 2013-12-22
| NUMBER OF SEQ ID NOS: 26415
| SEQ ID NOS: 26415
| SEQ ID NO 19156
| LENGTH: 201
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     77.8%; Score 200.6; DB 8; Length 201; 100.0%; Pred. No. 8.6e-53; ive 0; Mismatches 0; Indels 0
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Pred. No. 1.2e-52;
2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                            77.6%;
99.0%;
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Best Local Similarity 99.0
Matches 199; Conservative
                         al Similarity 100.
201; Conservative
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; ORGANISM: Homo sapiens
US-10-741-601-19156
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          Query Match
Best Local S
Matches 201
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                                                                                   44 AGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCA
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Publication No. US20040166519A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVERTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVERTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVERTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION UNDBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FASTSEQ for Windows Version 4.0
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Length 201;
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                                            Indels
  77.6%; Score 200.2; DB 8;
99.0%; Pred. No. 1.2e-52;
tive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 74.1%; Score 191.2; DB 7; Best Local Similarity 99.0%; Pred. No. 7.5e-50; Matches 190; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 51214, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
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Sequence 1, Application US/10220282A

Sequence 1, Application US/10220282A

Publication No. US20040053323A1

GENERAL INFORMATION:
APPLICANT: ISHII, YOSHINORI
APPLICANT: ISHII, YOSHINORI
APPLICANT: ARAKAWA, HIROYUKI
APPLICANT: NOTSU, YOSHINOM
FILE REFERENCE: 270899USOPT
CURRENT FILING DATE: 2003-05-21
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10

PRIOR FILING DATE: 2000-03-10

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 1

SEQ ID NO 1

LENGTH ARE
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                                   61 GGCTACCAGATGCCAGATGCCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
                                                                                   439 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 498
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46.7%; Score 120.4; DB 7;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1;
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Publication No. US20030092039A1
GENERAL INFORMATION:
APPLICANT: Olson-Munoz, Marilyn C.
APPLICANT: Donald, Glen
TITLE OF INVENTION: Screening Nutraceuticals
TITLE REFERENCE: PORS-07289
CURRENT APPLICATION NUMBER: US/10/210,682
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/309,279
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEC ID NOS: 8
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LUCATION: (1)..(3462); OTHER INFORMATION:
US-10-220-282A-1
                                                                                                                                       121 GT 122
                                                                                                                                                                                          499 CT 500
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NAME/KEY: CDS
LOCATION: (1).
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; Sequence 3, Application US/10220282A
; Publication No. US20040053323A1
; GENERAL INFORMATION:
APPLICANT: ISHII, YOSHINORI
APPLICANT: ISHII, YOSHITADA
; APPLICANT: NORIY
APPLICANT: NORSU, YOSHITADA
; TITLE OF INVENTION: SCREENING METHODS FOR INHIBITORS OF INDUCIBLE NITROGEN OXIDE SYNT
TITLE OF INVENTION: ACTIVATION
; TITLE OF INVENTION: ACTIVATION
; TITLE OF INVENTION: ACTIVATION
; FILE REFERENCE: 2278991050CT
; CURRENT APPLICATION NUMBER: US/10/220,282A
; CURRENT FILING DATE: 2001-03-09
; PRIOR FILING DATE: 2001-03-09
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 12
; SOFFWARE: Patentin version 3 1
APPLICANT: CARGILL, Michele et al.
TITLE OP INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT PELLING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 51214
LENGTH: 201
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                                                                                                                                                                                                                                                                                                                                                                         DB 8; Length 201;
                                                                                                                                                                                                                                                                                                                                                                    Query Match 74.1%; Score 191.2; DB 8; Length 3 Best Local Similarity 99.0%; Pred. No. 7.5e-50; Matches 190; Conservative 2; Mismatches 0; Indels
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Best Local Similarity 99.2
Matches 121, Conservative
                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-741-600-51214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                     TYPE: DNA
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Sequence 155, Application US/10631467
Sequence 155, Application US/10631467
Publication No. US20050208496A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive I TITLE OF INVENTION: Malease
FILE REFERENCE: 3462.1005-000
CURRENT APPLICATION NUMBER: US/10/631,467
CURRENT PILING DATE: 2003-07-31
PRIOR FILING DATE: 2003-07-20
PRIOR APPLICATION NUMBER: JP 2003-77212
PRIOR APPLICATION NUMBER: JP 2002-229312
PRIOR APPLICATION NUMBER: JP 2002-229312
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 2086
NUMBER OF SEQ ID NOS: 2086
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46.7%; Score 120.4; DB 9;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                           Score 120.4; DB 9;
Pred. No. 1.1e-27;
                                                                                                                                                                                                                                                                                                                     0; Mismatches
        PRIOR APPLICATION NUMBER: JP 2013-077212
PRIOR FILING DATE: 2003-03-20
PRIOR PLING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 2086
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 38
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; Sequence 228, Application US/10741601
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Best Local Similarity 99.2'
Matches 121; Conservative
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                                                                                                                                                                                          TYPE: DNA
COGANISM: Homo sapiens
US-10-631-467-38
CURRENT FILING DATE:
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TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720

CURRENT FILING DATE: 2002-11-26

PRIOR PRILICATION NUMBER: 09/016,434

PRIOR FILING DATE: 1998-01-30

NUMBER OF SEQ ID NOS: 1490

SOFTWARE: PERL PROGRAM

SEQ ID NO 1478

LENGTH: 4062
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TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive TITLE OF INVENTION: disease
FILE REFERENCE: 3462.1005-000
CURRENT APPLICATION NUMBER: US/10/631,467
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; OTHER INFORMATION: Genbank ID No. US20040010136A1 g951320
US-10-305-720-1478
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                                                                                                                                Query Match 46.7%; Score 120.4; DB 5
Best Local Similarity 80.3%; Pred. No. 1.1e-27;
Matches 98; Conservative 23; Mismatches 1
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                        LENGTH: 3855
TYPE: RNA
ORGANISM: Homo sapiens
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US-10-305-720-1478
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US-10-631-467-38
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      SEQ ID NO 1
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Publication No. US20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 20003-12-22
CURRENT FILING DATE: 20003-12-22
NUMBER OF SEQ ID NOS: 73397
SOFTWARE: FRASESQ for Windows Version 4.0
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Publication No. US20040166519A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1500
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26412
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 121; Conservative
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Matches 121; Conservative
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US-10-741-601-228
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CORGANISM: Homo sapiens
US-10-741-600-621
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US-10-741-600-621
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US-10-182-049-3; Sequence 3, Application US/10182049; Publication No. US20050113322A1

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APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: C. Frank Bennett
APPLICANT: Nicholas M. Dean
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION
FILE REFERENCE: RTSP-0360
CURRENT APPLICATION NUMBER: US/10/182,049
CURRENT FILING DATE: 2002-07-27
PRIOR APPLICATION NUMBER: 09/490,208
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 182
SEQ ID NO 3
LENGTH: 4145
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| Publication No. US20050113322A1
| Publication No. US20050113322A1
| GENERAL INFORMATION:
| APPLICANT: Isia Pharmaceuticals, Inc.
| APPLICANT: Nicholas M. Dean
| APPLICANT: Lax M. Cownert

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.7%; Score 120.4; DB 9;
99.2%; Pred. No. 1.1e-27;
tive 0; Mismatches 1;
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Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) NAME/KEY: CDS
; LOCATION: (207)...(3668)
US-10-182-049-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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US-10-182-049-10
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Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
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MEDIUM TYPE: RIOPPY disk
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC COMPATIble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: Unknown>
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                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE: 9441452
; SEQUENCE DESCRIPTION: SEQ ID NO: 1407
US-10-641-643-1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
                                                                                                                                                             Sequence 1407, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
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TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1407:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     APPLICANT: Cocks, Benjamin G.
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                    CITY: PALO ALTO STATE: CALIFORNIA
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                                                                       1071 CT 1072
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US-10-641-643-1407
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Sequence 622, Application US/10741600
| Publication No. US20050026169A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: CARGILL, Michele et al.
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
| TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
| FILE REFERENCE: CLO01499
| CURRENT APPLICATION NUMBER: US/10/741,600
| CURRENT FILING DATE: 2003-12-22
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Sequence 229, Application US/10741601

Publication No. US20040166519A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/741,601

CURRENT APPLICATION NUMBER: US/10/741,601

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 229

LENGTH: 4221
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NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.2%;
Matches 121; Conservative
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Best Local Similarity 99.2%;
Matches 121; Conservative
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US-10-741-600-622
                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-741-601-229
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LENGTH: 4221
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RESULT

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Sequence 123, Application US/09870759
Patent No. US2002017551A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR PILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
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Sequence 123, Application US/09751708A
Sequence 123, Application US/09751708A
Sequence 123, Application US/09751708A
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35.5%; Score 91.6; DB 3;
Best Local Similarity 84.4%; Pred. No. 1.1e-18;
Matches 103; Conservative 0; Mismatches 19;
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) NAME/KEY: CDS
; LOCATION: (256)..(3690)
; OTHER INFORMATION:
US-09-870-759-123
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; LOCATION: (256)..(3690)
; OTHER INFORMATION:
US-09-751-708A-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Mus musculus
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TT 857
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                                                                                                                                    US-09-870-759-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3690
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LENGTH: 3690
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Publication No. US20050064483A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zang, Jingwu
APPLICANT: Anng, Jian
TITLE OF INVENTION: Multiple Sclerosis
FILE REFERENCE: HO-P02859US1
CURRENT APPLICANTION: Wultiple Sclerosis
FILE REFERENCE: HO-P02859US1
CURRENT APPLICANTION NUMBER: US 60/498,731
PRIOR FILING DATE: 2003-08-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.3
SEQ ID NOS: 34
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          Sequence 37, Application US/10688845
Publication No. US20040247578A1
GENERAL INFORMATION:
APPLICANT: Lotze, Michael T
APPLICANT: Lotze, Michael T
APPLICANT: Lotze, Michael T
TILE OF INVENTION: Methods And Reagents For Inducing Immunity
FILE REFERENCE: UPT-00.
CURRENT FILING DATE: 2003-10-15
PRIOR APPLICATION NUMBER: 60/418,865
PRIOR FILING DATE: 2002-10-15
PRIOR FILING DATE: 2002-10-15
SOFTWARE: Patentin version 3.1
SEQ ID NO 37
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Best Local Similarity 98.4%; Pred. No. 3.5e-27;
Matches 120; Conservative 0; Mismatches 2; Indels 0;
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ORGANISM: Homo sapiens
US-10-688-845-37
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ORGANISM: HUMAN
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1042 GGCTACCAGATGCCCGATGGCACCATCAGAGGGATGCTGCCACCTTGGAGTTCACCCAG 1101
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84.4%; Pred. No. 1.1e-18;
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Pred. No. 1.1e-18;
0; Mismatches 19;
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             PRIOR APPLICATION NUMBER: 09/650,884
PRIOR FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 100
LENGTH: 3690
   2004-09-08
                                                                                                                                                                                                                                                                    35.5%;
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Best Local Similarity 84.41
Matches 103; Conservative
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Matches 103; Conservative
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; NAME/KEY: CDS
; LOCATION: (256)...(3690)
US-10-182-049-18
                                                                                                                                                              FEATURE:
NAME/KEY: CDS
LOCATION: (256)..(3690)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Mus musculus
                                                                                                                        TYPE: DNA ORGANISM: Mus musculus
   CURRENT FILING DATE:
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Sequence 119, Application US/10428817A

Publication No. US20040214783A1

GENERAL INFORMATION:

APPLICATOR: TERMAN, David S

TILE REFERENCE: 38373-189118

CURRENT APPLICATION NUMBER: US/10/428,817A

CURRENT APPLICATION NUMBER: US 60/378,988

PRIOR FILING DATE: 2002-05-05

PRIOR FILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-15

PRIOR PILING DATE: 2002-06-15

PRIOR PRIOR APPLICATION NUMBER: US 60/406,697

PRIOR APPLICATION NUMBER: US 60/406,750

PRIOR APPLICATION NUMBER: US 60/415,310

PRIOR APPLICATION NUMBER: US 60/415,310

PRIOR APPLICATION NUMBER: US 60/415,400

PRIOR PILING DATE: 2002-10-01

PRIOR APPLICATION NUMBER: US 60/415,400

PRIOR PILING DATE: 2002-10-02

PRIOR PILING DATE: 2003-01-09

PRIOR FILING DATE: 2003-01-09

PRIOR FILING DATE: 2003-01-09

NUMBER OF SEQ ID NOS: 224

SOFTWARE PATENTIN VEFSION 3.2
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Sequence 100, Application US/10937758A
Sequence 100, Application US/1093758A
PUBLICATION No. US20050112141A1,
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVERTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE;
TILE REFERENCE: FILE REFERENCE 650884
CURRENT APPLICATION NUMBER: US/10/937,758A
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CAGCGGAGTGACGCGAAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGGTACGCT 1041
                                                                            GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
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Pred. No. 1.1e-18;
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Best Local Similarity 84.4%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (256)..(3690)
US-10-428-817A-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Mus musculus
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LENGTH: 3690
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Sequence 1477, Application US/10305720

Publication No. US20040010136A1

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.

TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression

TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression

CURRENT APPLICATION NUMBER: US/10/305,720

CURRENT FILING DATE: 2002-11-26

PRIOR APPLICATION NUMBER: 09/016,434

PRIOR APPLICATION NUMBER: 09/016,434

NUMBER OF SEQ ID NOS: 1490

SOFTWARE: PERL Program
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| Sequence 1. Application US/10475049A
| Publication No. US20050019854A1
| GENERAL INFORMATION:
| APPLICANT: Lajoix, Anne-Dominique
| APPLICANT: Lajoix, Anne-Dominique
| APPLICANT: Ribes, Gerard
| TITLE OF INVENTION: Novel Method For Screening Inhibitors of
| TITLE OF INVENTION: Associated Protein and the Protein Inhibiting Neuronal
| TITLE OF INVENTION: Associated Protein and the Protein Inhibiting Neuronal
| TITLE OF INVENTION: NUMBER: US/10/475,049A
| CURRENT APPLICANTON NUMBER: PS/10/475,049A
| CURRENT FILING DATE: 2002-04-17
| PRIOR FILING DATE: 2001-04-18
| PRIOR FILING DATE: 2001-04-18
| NUMBER OF SEQ ID NOS: 106
| SEQ ID NO 1
| LEGGTH A 290
971 GGCTACCAGATGCCCGATGGCACCATCAGAGGGGATGCTGCCACCTTGGAGTTCACCCAG 1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
OTHER INFORMATION: Genbank ID No. US20040010136A1 g951318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Matches 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1532 ATA 1534
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                                                                                                  121 GT 122
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US-10-305-720-1477
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LENGTH: 4079
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WS-10-631-467-1064

WS-10-631-467-1064

WS-10-631-631

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WS-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3991;
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Pred. No. 1.1e-18;
0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.5%; Score 91.6; DB 9;
84.4%; Pred. No. 1.1e-18;
tive 0; Mismatches 19;
                                                                                           Sequence 966, Application US/10631467
Publication No. US20050208496A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 84.4%;
Matches 103; Conservative
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ORGANISM: Mus musculus
US-10-631-467-966
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; ORGANISM: Mus musculus
US-10-631-467-1064
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US-10-305-720-1234
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Sequence 56987, Application US/09925065A

Publication No. US20050228172A9

GENERAL INFORMATION:
GENERAL INFORMATION:
ITTLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16
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0
                                                                                                   Length 4290;
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                                                                                                   Score 75.6; DB 8; Length 4
Pred. No. 1.2e-13;
0; Mismatches 29; Indels
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66.4%; Pred. No. 4.9e-08;
iive 1; Mismatches 40;
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; Sequence 8, Application US/10889121
; Publication No. US20040253685A1
                                                                                                        Query Match
Best Local Similarity 76.2%;
Matches 93; Conservative
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Best Local Similarity 66.44
Best Local 81; Conservative
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US-09-925-065A-56987
NAME/KEY: CDS
LOCATION: (1)...(4287)
OTHER INFORMATION:
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US-09-925-065A-56987
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PAPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.

TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic FILE REPRENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR PILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL PROGram
SEQ ID NO 1234
APPLICANT: Sessa, William C.
TITLE OF INVENTION: BASSA, WILLIAM C.
CURRENT PAPLICATION NUMBER: US/10/889,121
CURRENT PILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: BCT/USO0/09913
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 1999-04-16
PRIOR FILING DATE: 1999-04-16
SEQ ID NOS: 9
SOFTWARE: Patentin version 3.2
SEQ ID NO
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; OTHER INFORMATION: GenBank ID No. US20040010136A1 g189259
US-10-305-720-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54.8; DB 8;
Pred. No. 3.7e-07;
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65.6%;
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 80; Conserv
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Sequence 9, Application US/10889121;
Publication No. US20040253685A1;
GENERAL INFORMATION:
A PAPLICANT: Sessa, William C.
TITLE OF INVENTION: eNOS MUTATIONS USEFUL FOR GENE THERAPY AND THERAPEUTIC SCREENING
FILE REFERENCE: 044574-5046-01;
CURRENT APPLICATION NUMBER: US/10/889,121
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APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-186-99
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/299,918
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2002-06-14
PRIOR PRIOR APPLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 414
                                                                                               1 CAGCGGAGTGATGGCAAGCACGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT
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Score 54.8; DB 6; Length 4077; Pred. No. 3.7e-07; 0; Mismatches 42; Indels 0
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Pred. No. 3.7e-07;
0; Mismatches 42;
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APPLICANT: He, Yudong
APPLICANT: Linaley, Peter S.
APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 414, Application US/10342887
Publication No. US20040058340A1
GENERAL INFORMATION:
  Query Match
Best Local Similarity 65.6%;
Matches 80; Conservative
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Best Local Similarity 65.6
Matches 80; Conservative
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; ORGANISM: Homo sapiens
US-10-342-887-414
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US-10-889-121-9
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TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720

CURRENT FILING DATE: 2002-11-26

PRIOR FILING DATE: 1998-01-30

NUMBER OF SEQ ID NOS: 1490

SOFTWARE: PERL Program

SEQ ID NO 1369

LENGTH: 4035
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APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REPERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR PILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 414
LENGTH: 4077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g434699
US-10-305-720-1369
                                                                                                                                        ; Sequence 1369, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
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Publication No. US20030224374A1
GENERAL INFORMATION:
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DATABASE ENTRY DATE: 2001-06-18
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APPLICANT: He, Yudong
APPLICANT: Lineley, Peter
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
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Matches 80; Conservative
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PUBLICATION INFORMATION
                     CT 838
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US-10-305-720-1369
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                       837
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CURRENT FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: US 09/956,699
PRIOR PILING DATE: 2001-09-20
PRIOR PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-04-14
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VERSION 3.2
LENGTH: 4077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: December 13, 2005, 18:27:38 Job time : 798 secs
                                                                                                                                                           ; LENGTH: 4077
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-889-121-9
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November 2005

available for processing searches. generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now

applications make up the Published_Applications_Main databases. Newly published applications will appear in the Published_Applications_New databases; older published

:rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New) Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New). Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions I HIS PAGE BLANK (USPTO)

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Sequence 837, App
Sequence 43745, A
Sequence 43750, A
Sequence 63750, A
Sequence 62600, A
Sequence 671, Appl
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Sequence 74, Appl
Sequence 3, Appli
Sequence 60778, A
                                                                                                           December 13, 2005, 16:32:55; Search time 238 Seconds (without alignments) 405.271 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'pred. No. is the number of results predicted by chance to have a bcore greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence
Sequence
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Sequence 4
Sequence 6
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1: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-11-121-086-74
US-11-121-086-74
US-10-750-185-60778
US-10-750-185-43745
US-10-750-185-4375
US-10-750-185-6375
US-10-750-185-62600
US-10-750-185-62600
US-11-121-086-4
US-10-750-185-6551
US-11-121-086-20
US-11-121-086-20
US-11-121-086-20
US-11-121-086-20
US-10-750-185-5951
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                                                                                                                                                                                                                                                                                                                              3392430 seqs, 186927314 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                           OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                Searched:
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                                                                                                                   Run on:
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No.
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Sequence 6, Appli	•••	Sequence 61399, A	Sequence 56711, A	Sequence 33, Appl	Sequence 551, App	Sequence 44988, A	Sequence 483, App	Sequence 67, Appl	Sequence 66, Appl	Sequence 39, Appl	Sequence 1, Appli	Sequence 49, Appl	Sequence 48, Appl	Sequence 52, Appl	Sequence 66, Appl	Sequence 47, Appl	Sequence 20492, A	Sequence 32804, A	Sequence 381, App	Sequence 1, Appli
US-10-645-441-6	US-10-643-441-11 US-10-750-185-26897	US-10-750-185-61399	US-10-750-185-56711	US-10-392-234A-33	US-10-821-234-551	US-10-750-185-44988	US-10-131-826A-483	US-11-080-991-67	US-11-121-086-66	US-11-112-908-39	US-10-496-711-1	US-11-112-908-49	US-11-112-908-48	US-11-112-908-52	US-11-121-086-66	US-11-112-908-47	US-10-750-185-20492	US-10-750-185-32804	US-10-131-826A-381	US-11-121-086-1
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2333	3745	4226	1215	3132	792	2233	2498	4305	163162	179892	2085	149419	161726	161726	163162	166111	9	1934	2236	126552
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28.2	28.5	28.2	28	28	27.8	27.8	27.8	27.8	27.8	27.8	27.6	27.6	27.6	27.6	27.6	27.6	27.4	27.4	27.4	27.4
24	26.5	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45.
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us-10-713-137-1.rnpbn

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82 AGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGGTACCCGGCCCAGCCCTCAGCC 141
                                                                                                                                                                                                                                                                                                 US-11-121-086-74
; Sequence 74, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 3, Application US/11121086; Publication No. US20050266459A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 58.4%;
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.3 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 56.7%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168516
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US-11-121-086-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        862 GCAAAGAAATGCAAATTTACTCCTAAACTTTGAACCATAAAAACATTCCAGGCAATCAAG 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 TACCCGGCCCAGCCTCAGCCRCCGGCCATTGGGGCGGGGGGGCCCCGTGGTGAGCGAGTGA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 GACTICCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATGGC
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Sequence 5939.

Publication No. US20050260603A1

GENERAL INFORMATION:

APPLICANT: MI GENOMICS, INC.

APPLICANT: MAI GENOMICS, INC.

APPLICANT: MAI GENOMICS, INC.

APPLICANT: MAI GENOMICS, INC.

APPLICANT: FART, Richard

APPLICANT: HOLM, Tom

APPLICANT: HOLM, Tom

APPLICANT: FAATIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MAII100-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

PRIOR PELLING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PALENTIN VERSION 3.1

LENGTH: 2827
                                                                                                                                                                                                                                                                           NAME/KEY: primer bind
LOCATION: 1842..1862
OCHER INFORMATION: downstream amplification primer, complement
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.7%; Score 32.8; DB 7; Length 3001; Best Local Similarity 51.4%; Pred. No. 1.7; Matches 76; Conservative 0; Mismatches 72; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32.2; DB 6; Length 2827; Pred. No. 2.4; 0; Mismatches 123; Indels 0
                                                                              FEATURE:
NAME/KEY: misc_binding
LOCATION: 1502. 1520
OTHER INFORMATION: 99-26223-225.mis2, complement
                                                                                                                                                                 FEATURE:
NAME/KEY: primer bind
LOCATION: 1277..1297
OTHER INFORMATION: upstream amplification primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 CAGAGTGGAGCCCAGAGGAGACACGCAG 209
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_binding
LOCATION: 1489..1513
OTHER INFORMATION: 99-26223-225 probe
US-11-145-703-194
                                          LOCATION: 1481...1500
OTHER INFORMATION: 99-26223-225.mis1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Bovine 19866880650684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ucery match
Best Local Similarity 46.3%;
Matches 106; Conservative
                 NAME/KEY: misc binding LOCATION: 1481..1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-750-185-59391
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                                                                         APPLICANT: POULSEN, TIM S.
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OP INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT APPLICATION NUMBER: US/11/121,086
PRIOR APPLICATION NUMBER: 06/567,570
PRIOR PILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
SEQ ID NO 74
LIENGTH.154452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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APPLICANT: POULSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILLING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                   1194 GCAGGCATGACAGGCAAGGTGCTGGACACCGCCCATGCAGGCCTTCATC 1242
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                                                                                                                                                                                                       202 ACACGCAGCCCGGGCTTACAGACTCACAGGCCCCGTCTTGTTCCCCAGC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 7; Length 168516; Pred. No. 7.7; 1; Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 7; Length 154452; 
Pred. No. 7.7; 
1; Mismatches 36; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117927 rccadccacacacadaaacacacaca 117955
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0; Mismatches 47; Indels
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                                                                                                                                                                                                                                                                                          DB 6;
10;
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Publication No. US20050260659A1
GENERAL INFORMATION:
APPLICANT: Hars, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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Pred. No. 11
PRIOR FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: US 60/531,596
PRIOR FILING DATE: 2003-12-19
PRIOR APPLICATION NUMBER: US 60/562,417
PRIOR FILING DATE: 2004-04-14
NUMBER OF SEQ ID NOS: 2184
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 837
                                                                                                                                                                                                                                                                                             Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 43745
LENGTH: 1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Bovine 19866880599390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.6%;
55.2%;
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 52.5%;
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58; Conservative
                                                                                                                                                                                                       TYPE: DNA
CORGANISM: H. sapiens
US-10-909-125-837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                    LENGTH: 4745
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APPLICANT: Dain, Ravi
APPLICANT: Bhat, Balkrishen
APPLICANT: Bratta, Eigen
APPLICANT: Bratta, Eigen
TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
TITLE OF INVENTION: OS Small Non-Coding RNAs
FILE REPERENCE: ISISO808-100 (COREO16US)
CURRENT APPLICATION NUMBER: US/10/909,125
CURRENT FILING DATE: 2004-07-30
PRIOR APPLICATION NUMBER: US 60/492,056
PRIOR FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US 60/516,303
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0
                                                                                                                                                                                                                   Sequence 60778, Application US/10750185

publication No. US20050260603A1

j GENERAL INPORMATION:

APPLICANT: MAI GENOMICS, INC.

APPLICANT: DeNISE, Sue K.

APPLICANT: RESERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: BATES, Stephen

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

TITLE OF INVENTION: COMPOSITIONS (00/437,482)

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

PRIOR PILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PALENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.9%; Score 30.6; DB 6; Length 2840; Best Local Similarity 60.8%; Pred. No. 6.8; Matches 48; Conservative 1; Mismatches 30; Indels 0
                                                                                                                   98331 gcaegererececeacadaeceacaceceacece
                                                                            181 ACAGAGTGGAGCCCAGAGGAGACACGCAGCCCGGGCT
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APPLICANT: Lollo, Bridget
APPLICANT: Bennett, C. Frank
APPLICANT: Freier, Susan M.
APPLICANT: Griffey, Richard H.
APPLICANT: Baker, Brenda F.
APPLICANT: Vickers, Timothy
APPLICANT: Marcusson, Eric G.
APPLICANT: Koller, Erich
APPLICANT: Swayze, Eric
                                                                                                                                                                                                            US-10-750-185-60778/c
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LENGTH: 2840
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66 CCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGGTACC 125
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                                                                                                               53 GCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAAT 112
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i Sequence 43745, Application US/10750185

j Sequence 43745, Application US/10750185

j Publication No. US20050260603A1

j GENERAL INFORMATION:

j APPLICANT: Denise K.

j APPLICANT: ROSENFELD, David

j APPLICANT: ROSENFELD, David

j APPLICANT: PANTIN, Demis

j TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MM1100-2

j CURRENT APPLICATION NUMBER: US/10/750,185

j CURRENT FILING BATE: 2003-12-31

CURRENT FILING BATE: 2003-12-31

CURRENT FILING BATE: 2003-12-31

CURRENT FILING BATE: 2003-12-31
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Length 4745;
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218 TACAGACTCACAGGGCCCGTCTTGTTCCCCAGC
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US-10-750-185-31860
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US-10-750-185-62600
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Best Local Similarity
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APPLICANT: KERR, Richard
APPLICANT: ROSENPELD, David
APPLICANT: ROSENPELD, David
APPLICANT: ROSENPELD, David
APPLICANT: BATES, Stephen
APPLICANT: PANTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT FILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 29.8; DB 7; Length 1
Pred. No. 17;
1; Mismatches 88; Indels
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FILE REFERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR PELING DATE: 2004-04-3
PRIOR PELING DATE: 2004-06-01
PRIOR PELING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR FILING DATE: 2004-11-30
PRIOR PELING DATE: 2004-11-30
PRIOR PELING DATE: 2004-11-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: PATCHING DATE: 2004-12-07
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US-10-750-185-63750/c
; Sequence 63750, Application US/10750185
; Publication NO. US20050260603A1
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ORGANISM: Bovine 19866880851319
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48.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 48.0°
Matches 82, Conservative
                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                      SEQ ID NO 38
LENGTH: 171162
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LENGTH: 1009
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64 TACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGGTA 123
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                                                                                                                                                        US-10-750-185-31860/c

| Sequence 31860, Application US/10750185 |
| Sequence 31860, Application US/10750185 |
| Publication No. US20050260603A1 |
| GENERAL INFORMATION: |
| APPLICANT: MIGHOMICS, INC. |
| APPLICANT: RERR, Richard |
| APPLICANT: ROSENFELD, David |
| APPLICANT: ROSENFELD, David |
| APPLICANT: PATEN, Exphen |
| APPLICANT: PATEN, Dennis |
| TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS |
| FILE REFERENCE: MAILION-2 |
| CURRENT APPLICATION NUMBER: US/10/750,185 |
| CURRENT APPLICATION NUMBER: US 60/437,482 |
| PRIOR FILING DATE: 2002-12-31 |
| NUMBER OF SEQ ID NOS: 64922 |
| SEQ ID NO 31860 |
| LENGTH: 1676 |
| LENGTH
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Sequence 62600, Application US/10750185

Publication No. US20050260603A1

GENERAL INFORMATION:
APPLICANT: WMI GENOMICS, INC.
APPLICANT: BOSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT PILING DATE: 2003-12-31
FRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 62600
LENGTH: 3138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 3138;
662 recrerandendendendenteccenden 630
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55.7%; Pred. No. 15;
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11.2%;
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SOFTWARE: PatentIn version 3.3
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Best Local Similarity 49.7
Matches 71; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Homo sapiens
US-10-821-234-671
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US-10-821-234-671
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                                                                                                                                      1370 GCTACACCTCCTCCCAGCTGCCATTTTTTCTGCAAGTGCAGAAACTGCCAGTGAGGCAG 1311
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                                                                   53 GCTATGCTGGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAAT 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/11121086
; Sequence 4, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
    APPLICANT: POULSEN, TIM S.
; APPLICANT: POULSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT PILING DATE: 2005-05-04
; PRIOR FILING DATE: 2005-05-04
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ IN NOS: 107
; SOFTWARE: PALENTIN VERSION 3.3
; SEQ ID NO 4.2007
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 67, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
TITLE OF INVENTION:
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT PELLON DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 67
LIBRITH: 179666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Gaps
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Pred. No. 22;
1; Mismatches 47; Indels
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42; Indels
                                                                                                                                                                                                                                                                                   1310 CAGAAGCAACACCAGCAGAGCCTCAGCCAATGCACA 1274
                                                                                                                                                                                                                113 TCACTCAGGTACCCGGCCCAGCCTCAGCCRCCGGCCA 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29.2; DB; Pred. No. 24; 0; Mismatches
   1; Mismatches
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57.8%;
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Best Local Similarity 54.3%;
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52; Conservative
       54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-121-086-67/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
       Matches
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| Publication No. US20050255114A1
| Publication No. US20050255114A1
| GENERAL INFORMATION:
| APPLICANT: Stache-Crain, Birgit
| APPLICANT: Andarmani, Susan
| APPLICANT: Andarmani, Susan
| APPLICANT: Andarmani, Susan
| APPLICANT: Andarmani, Susan
| TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
| TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
| TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
| TITLE OF INVENTION: UNMBER: US/00462,047
| PRIOR APPLICATION NUMBER: US 60/462,047
| PRIOR APPLICATION NUMBER: US 60/462,047
| SOFTWARE: pt. SEQ_genes Version 1.0
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Sequence 20, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: POULSEN, TIM S.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT PILLING DATE: 2005-05-04
PRIOR FILLING DATE: 2004-05-04
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Pred. No. 19;
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Pred. No. 27;
0; Mismatches
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1394 GCGGGTGGCCTGGTGGCTGAGGGGATGGATGACCTGAGGGGGCCTTCCAGGTGGC 1335
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                                                                                                                                                                               408 AGCAGCCGAGGCCTGGGACCGTGCGCGGGACTGCCTCTAGGGCCCGGCCCTGCCCCAGCC
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Sequence 54914, Application US/10750185

Publication No. US20050260603A1

GENERAL INFORMATION:

APPLICANT: MM GENOMICS, INC.

APPLICANT: MERR Richard

APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, David

APPLICANT: PANTIN, Dennis

TITLE OF INVENTIN, Dennis

TITLE OF INVENTIN, Dennis

FILE REFERENCE: MAILING-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT APPLICATION NUMBER: US 60/437,482

PRIOR PILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SEQ ID NO 54914

LENGTH: 861
                                                                    Score 28.8; DB 6; Length 1564;
Pred. No. 20;
0; Mismatches 47; Indels 0
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APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR PELING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                               1334 GCTGAGGGCCTGAAGGGGACCATCTTGTCTACCTGAGGTTCCTC 1291
                                                                                                                                                                                                                                                                             215 GCTTACAGACTCACAGGGCCCGTCTTGTTCCCCCAGCTGTGCATC 258
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Bovine 19866881313891
US-10-750-185-54914
ORGANISM: Bovine 19866880936088
                                                                            11.2%;
54.8%;
                                                                                                                           57; Conservative
                                                                                              Best Local Similarity
Matches 57; Conserv
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108108 CTCAGCCCCTCACCTGGCAGCCTGTTGCCCTGTGCCCCTCAGTGAGGAGACGAGGTCAT 108049
                                                                                                   106 GIGGAATICACICAGGIACCCGGCCCAGCCICAGCCRCCGGCCATIGGGGCGGGGGGGCCC 165
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APPLICANT: KERR, Richard
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TILLE OF INVENTION: COMPOSITIONS FOR INPERRING BOVINE TRAITS
TILLE REFERENCE: MAILOO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR RILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.

APPLICANT: ENGINER, Richard

APPLICANT: ERRR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: BOSENFELD, David

APPLICANT: APPLICANT: APPLICANTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: US 60/437,482

MIMMED OF SEC IN MAG. 2402-12-31
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Pred. No. 18;
1; Mismatches 38; Indels
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Publication No. US20050260603A1
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Publication No. US20050260603A1
                                                                                                                                                     CGTGGTGAGCGAGTGACAGAG 186
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SOFTWARE: PatentIN version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 56.7%;
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                 FUDITCALL...
GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Bovine MMBT07408
US-10-750-185-868
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US-10-750-185-56551/c
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US-10-750-185-868/c
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LENGTH: 1564
TYPE: DNA
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NUMBER OF SEQ ID NOS: 107
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Publication No. US20050266459A1
Publication No. US20050266459A1
APPLICANT: NIGHTON:
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
FILLE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
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APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: PATIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILLOO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT PILING DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 25939
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                                                                                                                                             Score 28.6; DB 6;
Pred. No. 22;
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Pred. No. 23;
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Publication No. US20050260603A1
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                       PatentIN version 3.1
                                                                                                                                               Query Match
Best Local Similarity 53.2%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: MMI GENONICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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nes 58; Conserva
                                                                        ; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-34965
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US-10-750-185-25939
NUMBER OF SEQ ID N
SOFTWARE: PatentIN
SEQ ID NO 34965
LENGTH: 1196
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APPLICANT:
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APPLICANT: MINGGENOMICS, INC.
APPLICANT: ERRR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: FAUNTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
GURRENT PAPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 64922
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Pred. No. 36;
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US-10-750-185-45463
US-10-750-185-4643
Sequence 45463, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                 11.1%;
50.8%;
SOFTWARE: PatentIn version 3.3 SEQ ID NO 105
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Matches 80; Conserv
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                                                                                                                    LENGTH: 171486
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US-11-121-086-6/c
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                              158 GGGAGCCCCGTGGTGAGCGAGTGACAGAGTGGAGCCCCAGAGGAGACACGCAGCCCGGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang, Yifeng
The Regents of the University of California
The Government of the United States of America
as represented by the Secretary of the
Department of Health and Human Services
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Mammalian Sweet Taste Receptors PILE REFERENCE: 02307E-120110US CURRENT APPLICATION NUMBER: US/10/645,441 CURRENT FILING DATE: 2003-08-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: mouse T1R2 sweet taste receptor
US-10-645-441-11
                                                                                                                                                                          1705 AGCAAGCACGCAGGCCTTGTGGGTTCCCCAA 1675
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PRIOR PILING DATE: 2003-08-20
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/302,898
PRIOR FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 11
                                                                                                                          218 TACAGACTCACAGGGCCCGTCTTGTTCCCCA
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Publication No. US20050260603A1
Publication No. US20050260603A1
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DEMYSE, SUR K.
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                          Sequence 11, Application US/10645441 Publication No. US20050260599A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  Nelson, Greg
Hoon, Mark A.
Chandrashekar, Jayaram
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APPLICANT: Ryba, Nicholas J.P.
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APPLICANT:
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APPLICANT: POULSEN, TIM S.

APPLICANT: POULSEN, KTRSTEN V.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE OF INVENTION: NUCLEIC ACID PROBES FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zhang, Yifeng
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Mammalian Sweet Taste Receptors
FILE REFERENCE: 02307E-120110US
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                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/645,441
CURRENT FILING DATE: 2003-08-20
PRIOR PELING DATE: 2003-08-30
PRIOR FILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zuker, Charles S.
APPLICANT: Ryba, Nicholas J.P.
APPLICANT: Nelson, Greg
APPLICANT: Hoon, Mark A.
APPLICANT: Chandrashekar, Jayaram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/10645441 Publication No. US20050260599A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 66.1
Matches 41; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
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APPLICANT:
APPLICANT:
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SEQ ID NO 33
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Best Local
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US-10-750-185-61399/C
Sequence 61399, Application US/10750185
Sequence 61399, Application US/10750185
Publication No. US20050260603A1
SEQUENCE INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: RERR, Richard
APPLICANT: ROSNFELD, David
APPLICANT: BATES, Stephen
APPLICANT: PAPLICANT: POINTIN, Dennis
APPLICANT: PAPLICANT: PAPLICANT:
APPLICANT: PAPLICANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAII100-2
CURRENT FILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
NUMMEP OR SEC TO NUMBER: US 60/437,482
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAIL100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 26897
LENGTH: 3745
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Pred. No. 32;
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US-10-750-185-56711
Sequence 56711, Application US/10750185
; Publication No. US20050260601A1
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US-10-750-185-26897
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llarity 70.6%;
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SOFTWARE: PatentIN version 3.1
SEQ ID NO 61399
LENGTH: 4226
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Best Local Similarity 52.1%;
Matches 63; Conservative
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Best Local Similarity
Matches 36; Conserv
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US-10-750-185-61399
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APPLICANT: Buxser, Steven
APPLICANT: Poole, Keith
APPLICANT: Poole, Keith
APPLICANT: Decker, Duglas
APPLICANT: Decker, Duglas
APPLICANT: APPLICANT STATCH IN
TITLE OF INVENTION: Method for Screening for acrAB Transporter Family Inhibitors
FILE REFERENCE: 6206
FURRENT APPLICATION NUMBER: US/10/392,234A
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US 60/364,935
PRIOR FILING DATE: 2002-03-15
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Pred. No. 33;
1; Mismatches 66; Indels
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Pred. No. 36;
0; Mismatches 90; Indels
                                                   APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATTN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILION-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT PILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-392-234A-33
; Sequence 33, Application US/10392234A
; Publication No. US20050255538A1
GENERAL INFORMATION:
; APPLICANT: Pharmacia and Upjohn Corporation
                                                                                                                                                                                                                                            CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Bovine 19866880824999
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1 Similarity 47.7%;
82; Conservative
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SOFTWARE: PatentIN version 3.1
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Best Local Similarity 50.0%;
Matches 67; Conservative
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SOFTWARE: PatentIn version 3.1
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DeNISE, Sue K.
KERR, Richard
ROSENFELD, David
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT APPLICATION NUMBER: 60/49911
PRIOR PAPLICATION NUMBER: 60/05911
PRIOR PELING DATE: 1997-06-18
PRIOR PELING DATE: 1997-06-26
PRIOR PELING DATE: 1997-06-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-19
                                                                                                                                                                                                                                             1380 CCTGCAGTGCAGGAGATCCAGACAACATGGGTTTGACCCCTGGGTCGGGAAGAGCCCCTG 1321
                                                                             1440 ATGAGTACAAGGTACCTAAGTTCCTGGGCTTCCCCGATGGCTCAGCAGGTAAGAATTCTG 1381
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20 ACGACTICCGGGTGTGCAATGCTCAGCTCATCCGCTATGCTGGCTACCAGATGCCAGATG
                                                                                                                                                                80 GCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGGTACCCGGCCCAGCCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
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Pred. No. 40;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5-10-131-826A-483
Sequence 483, Application US/10131826A
Publication No. US20050245730A1
GENERAL INPORMATION:
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1320 GAGGAGGCCATTGTGAC 1304
                                                                                                                                                                                                                                                                                                                                140 CCRCCGGCCATTGGGGC 156
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Best Local Similarity 54.6%;
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith, Victoria
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumas, Daniel
Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-826A-483
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Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani

APPLIC
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303 CCTGGCCCAGGTGGACGTGCAGAACCGCCTGAAGAAAGCCGAGGCGCGCATGCCGCAGGC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                             201 GACACGCAGCCCTTACAGACTCACAGGCCCCGTCTTGTTCCCCAGCTG 252
                                                                                                                                                           363 GGTGCTGACCCAGGCCTGCAGGTCGAGCAGACCAGCGCCGGTTTCCTGCTG 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.8%; Score 27.8; DB 6; Length 2233; 49.6%; Pred. No. 40; tive 1; Mismatches 68; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.8%; Score 27.8; DB 6; Length 792; Best Local Similarity 54.6%; Pred. No. 36; Matches 53; Conservative 1; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 AGACACGCAGCCCGGGCTTACAGACTCACAGGGCCCG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 ccaccrecaeccreerecrecaeacrearereacee 173
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: CENC.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Bovine 19866880984581
US-10-750-185-44988
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ORGANISM: Homo sapiens
US-10-821-234-551
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Best Local Similarity
Matches 68; Conservat
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Sequence 1, Application US/10496711

Sequence 1, Application US/10496711

Sequence 1, Application No. US20050256649A1

GENERAL INFORMATION:

TITLE OF INVENTION: HIGH THROUGHPUT CORRELATION OF

TITLE OF INVENTION: POPULATIONS WITH MULTIPLE PHENOTYPES WITHIN CLINICAL

TITLE OF INVENTION: POPULATIONS

FILE REPERENCE: PU4699WO

CURRENT APPLICATION NUMBER: US/10/496,711

CURRENT PILING DATE: 2004-05-26

PRIOR PAPLICATION NUMBER: 60/344992

PRIOR PILING DATE: 2002-12-21

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PSECSE FOR Windows Version 4.0

SEQ ID NO 1

LENGTH: 2085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 10.8%; Score 27.8; DB 7; Length 179892; al Similarity 54.6%; Pred. No. 59; 53; Conservative 1; Mismatches 43; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 CAGAGTGGAGCCCAGAGGAGACACGCAGCCCGGGCTT 218
                                                                                                                                                                                                                                                                                                                              APPLICANT: Harris, Cole
APPLICANT: Harris, Cole
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR PILING DATE: 2004-11-30
PRIOR PILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-12-07
NUMBER OF SEQ 1D NOS: 511
                                                                                                                                                                                                                                                       Sequence 39, Application US/11112908; Publication No. US20050260659A1; GENERAL INFORMATION:
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56.7%;
                                                                                                                              32865 AGCACAGCCTC 32875
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Best Local Similarity 56.7
Matches 51, Conservative
                                                                                 127 GGCCCAGCCTC 137
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; ORGANISM: Homo Sapiens
US-10-496-711-1
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Best Local Similarity
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
TITLE OF INVENTION: AND OVARIAN CANCER
FILE REFERENCE: MRI-039
CURRENT APPLICATION NUMBER: US/11/080,991
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: US/10/176,847
PRIOR APPLICATION NUMBER: US/10/176,847
PRIOR SEQ ID NOS: 112
NUMBER OF SEQ ID NOS: 112
SOFTWARR: FASTSEQ for Windows Version 4.0
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     79 GCCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAGGTACCCGGCCCAGCCTCA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            687 grchrchcchgecrachecedecchesecretrecrashssesersesedecereseden
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APPLICANT: POULSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR PRILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PATENTIN version 3.3
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1; Mismatches 63; Indels 0
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                                                                                                                                   153 ccaccrecaeccreerecrecaeacrearereacee 189
                                                                                    200 AGACACGCAGCCCGGGCTTACAGACTCACAGGGCCCG 236
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Publication No. US20050266459A1
GENERAL INFORMATION:
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Best Local Similarity 50.4%;
Matches 65; Conservative 1
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US-11-121-086-66
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LENGTH: 163162
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US-11-121-086-66
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98434 GAAĞCCGGCGGCCTTCCCTCCGCAGAGGCACGAGGGCCGCCACGACGGAGGGTGGCTCG 98375
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Pred. No. 67;
1; Mismatches 105; Indels
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Pred. No. 67;
1; Mismatches 105;
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Publication No. US2005026659A1
GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/55,978
PRIOR FILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-07
NUMBER OF SEQ ID NOS: 511
SCOFWARE: PatentIn version 3.3
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR FILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: Patentin version 3.3
SEQ ID NO 48
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45.9%;
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ilarity 45.9%;
Conservative
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Best Local Similarity 45.3.
Thea 90; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 90; Conserva
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SEQ ID NO 52
LENGTH: 161726
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                                               126 CGGCCCAGCCTCAGCCRCCGGCCATTGGGGCGGGGAGCCCCGTGGTGAGCGAGTGACAGA 185
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Publication No. US20050260659A1
GENERAL INPORMATION:
APPLICANT: Harris, Cole
APPLICANT: Harris, Cole
TITLE OF INVENTION:
FILE REFERENCE: 04-164 US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
FRIOR PELLOATION NUMBER: US 60/564,758
FRIOR APPLICATION NUMBER: US 60/575,978
FRIOR APPLICATION NUMBER: US 60/575,978
FRIOR FILING DATE: 2004-06-01
FRIOR FILING DATE: 2004-11-30
FRIOR FILING DATE: 2004-11-30
FRIOR FILING DATE: 2004-11-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: PATENTIN VOTEION 3.3
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APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REPERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-06-01
PRIOR FILING DATE: 2004-06-01
                                                                                                                                                                                                                                                                          1512 CTCTCGGCTCTCGGCCCCCGCGCCTCTGGG 1483
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Publication No. US20050260659A1
GENERAL INFORMATION:
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Matches 90; Conserv
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US-11-112-908-49/c
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US-11-112-908-49
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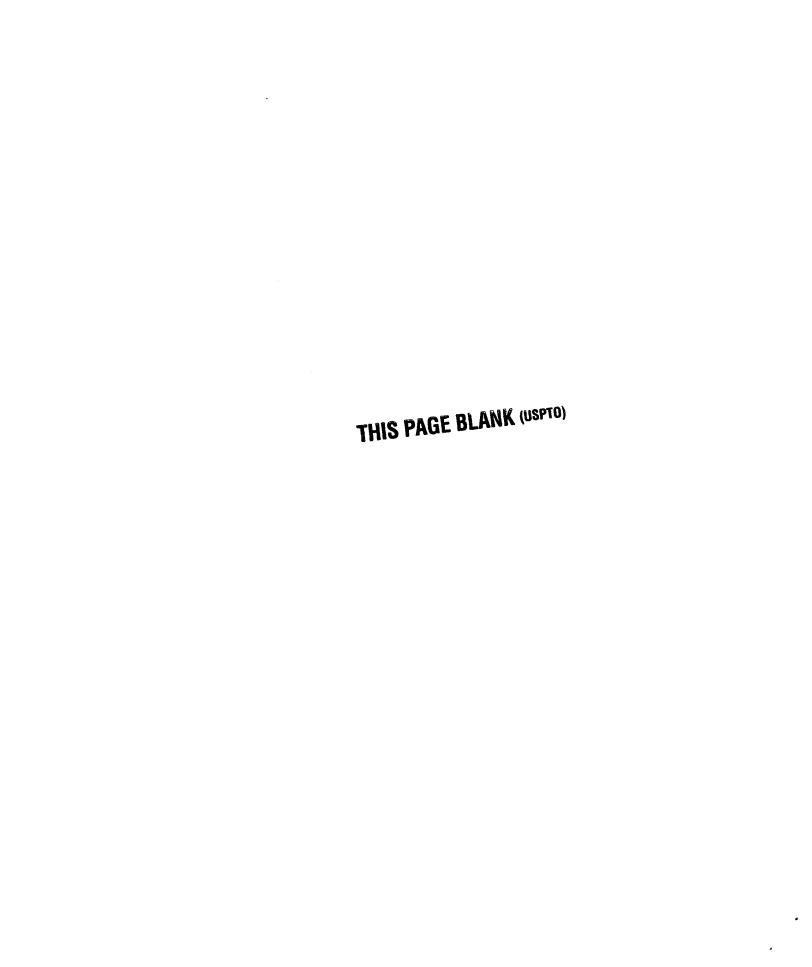
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98434 GAAGCCGGCGGCCTTCCCTCCGCAGAGGCACGACGCCCCCACGACGGAGGGTGGCTCG 98375
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                                                                                                                                                                                                             Sequence 66, Application US/11121086
Sequence 66, Application No. US20050266459A1
GENERAL INFORMATION;
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES;
FILE REFERENCE: 09138, 6000-00000;
CURRENT FILING DATE: 2006-005-004;
PRIOR APPLICATION NUMBER: 05/567,570
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR PILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 66
LENGTH: 163162
TYPE: DNA
CORGANISM: Homo sapiens
US-11-121-086-66
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Best Local Similarity 51.6%; Pred. No. 67;
Matches 63; Conservative 0; Mismatches 59; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: December 13, 2005, 18:31:57 Job time: 249 secs
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US-11-121-086-66/c
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Sequence 267621,
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Sequence 18164, A
Sequence 181892,
Sequence 189892,
Sequence 55223,
Sequence 520337,
Sequence 520337,
Sequence 18105,
Sequence 18105,
Sequence 18105,
Sequence 27338,
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Sequence 336028,
Sequence 368993,
Sequence 372996,
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Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pasha, Abdul Qadar Mohammad
APPLICANT: Pasha, Abdul Qadar Mohammad
APPLICANT: Pasha, Abdul Qadar Mohammad
TITLE OF INVENTION: A method of detection of predisposition
TITLE OF INVENTION: to high altitude pulmonary edema (HAPE)
FILE REFERENCE: 09755-0018U31
CURRENT APPLICATION NUMBER: US/10/713,137
CURRENT FILING DATE: 2003-11-13
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 24; DB 9; Length 24; 100.0%; Pred. No. 0.38;
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CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991774
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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US-11-036-317-483105
US-11-036-317-27344
US-11-036-317-27228
US-11-036-317-316163
US-11-036-317-36028
US-11-036-317-372996
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US-11-036-317-89892
US-11-036-317-55223
US-11-036-317-770140
US-10-349-143-1997
US-10-719-900-520335
US-10-719-900-520337
US-10-719-956-198953
US-10-719-956-198954
US-10-719-900-58299
US-10-719-900-267621
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US-10-956-157-14604
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Publication No. US20050106573A1
GENERAL INFORMATION:
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                                         24; Conservative
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Matches 24; Conserv
    RESULT 2
US-11-036-317-523844
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    SEQ ID NO 3
LENGTH: 24
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Sequence 83698, A
Sequence 743593,
Sequence 904575,
Sequence 979803,
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                                                                                                                                         December 13, 2005, 13:21:57; Search time 660 Seconds (without alignments) 300.705 Million cell updates/sec
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| /cgn2 6/ptcdata/1/pubpna/US08 PUBCOMB.seq:*
| /cgn2 6/ptcdata/1/pubpna/US08 PUBCOMB.seq:*
| /cgn2 6/ptcdata/1/pubpna/US08 PUBCOMB.seq:*
| /cgn2 6/ptcdata/1/pubpna/US108 PUBCOMB.seq:*
                          GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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0 US-10-719-900-641215

0 US-11-036-317-523845

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US-10-719-900-83698
US-10-719-900-943593
US-10-719-900-904575
US-10-719-900-90803
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Maximum Match 100%
Listing first 45 summaries
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                                               Copyright
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US-10-719-900-743593/c
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LENGTH: 25
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US-10-719-956-683762/c

Sequence 683762, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INPORMATION:
APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REPERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002 11 20
; PRIOR FILING DATE: 2002 11 20
; NUMBER: OF SEQ ID NOS: 699466
; SOFFWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
                                                                                                                      Query Match 70.0%; Score 16.8; DB 10; Length 25; Best Local Similarity 90.0%; Pred. No. 8e+02; Matches 18; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.8%; Score 15.8; DB 8; Length 25; Best Local Similarity 89.5%; Pred. No. 2.3e+03; Matches 17; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.8%; Score 15.8; DB 7; Length 25; 89.5%; Pred. No. 2.3e+03;
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REPERENCE: 35.20
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT PILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR PILING DATE: 2002 11 20
PRIOR FILING DATE: 2002 11 20
PRIOR FILING SEQ ID NOS: 98.214
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
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US-10-719-956-683762
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US-10-719-900-83698
                                         TYPE: DNA
CORGANISM: Mus musculus
US-11-036-317-523844
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; SEQ ID NO 523844
; LENGTH: 25
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LENGTH: 25
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                     LENGTH:
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US-10-719-900-979803/Application US/10719900
; Sequence 979803, Application No. US20050026164A1
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TILE REFERENCE: 3528.1
; CURRENT PAPLICATION NUMBER: US/10/719,900
; CRRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FLING DATE: 2002-11 20
; NUMBER OF SEQ ID NOS: 922914
; SOFFWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 979803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 904575. Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mai Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse;
FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2003-11-20
; NUMBER OF SEQ ID NOS: 982914
; SEQ ID NO 904575
; LENGTH: 25
Sequence 743593, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFRENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: US/10/719,900
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2003-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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Pred. No. 2.3e+03;
0; Mismatches 2;
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89.5%;
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Best Local Similarity 89.54
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Best Local Similarity 89.5.
Best Local 7; Conservative
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; ORGANISM: Mus musculus
US-10-719-900-904575
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US-10-719-900-743593
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TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 18; Conservative
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Best Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus US-11-036-317-810975
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US-10-874-242-35
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TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse FILE REFERENCE: 3654.11
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT PILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 296939
LENGTH: 25
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APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
                                                                                                                                          Gaps
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                                                                                               Score 15.8; DB 8; Length 25;
Pred. No. 2.3e+03;
0; Mismatches 2; Indels
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PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ IN NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
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Pred. No. 2.9e+03;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                        ; Sequence 296939, Application US/11036317; Publication No. US20050214823A1; GENERAL INFORMATION:
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Publication No. US20050214823A1
GENERAL INFORMATION:
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                                                                                               Ouery Match
Best Local Similarity 89.5%;
Matches 17; Conservative (
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Best Local Similarity 81.8%;
Matches 18; Conservative
                   TYPE: DNA
CORGANISM: Mus musculus
US-10-719-900-979803
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; ORGANISM: Mus musculus
US-11-036-317-296939
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LENGTH: 25
LENGTH: 25
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), OTHER INFORMATION: forward primer for amplifying beta-actin promoter containing; OTHER INFORMATION: intron 1
US-10-874-242-35
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Sequence 810975, Application US/11036317
; Sequence 810975, Application No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 364.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 810975
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
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APPLICANT: ZHANG, WEIGUN
TITLE OF INVENTION: NOVEL PROMOTERS AND USES THEREOF
FILE REFERENCE: 07680.0027-00000
CURRENT APPLICATION NUMBER: US/10/874,242
CURRENT FILING DATE: 2004-06-24
PRIOR APPLICATION NUMBER: 60/480,768
PRIOR APPLICATION NUMBER: 60/480,768
PRIOR PILING DATE: 2003-06-24
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
SEQ ID NO 35
LENGTH: 26
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81.8%; Pred. No. 2.9e+03;
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
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Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative
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LENGTH: 25
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| Publication No. US20050026164A1
| GENERAL INFORMATION:
| APPLICANT: We Mei Zhou
| TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
| TITLE OF INVENTION: Wethods of Genetic Analysis of Mouse
| TITLE OF INVENTION: Wethods of Genetic Analysis of Mouse
| CURRENT APPLICATION NUMBER: 05/10/719,900
| CURRENT FILING DATE: 2003-11-20
| PRIOR PRILIG DATE: 2002-11-20
| WUMBER OF SEQ ID NOS: 982914
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| LENGTH: 25
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CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427, 808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 741411
LENGTH: 25
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Publication No. US20050048531A1
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
CURRENT APPLICANTON NUMBER: US/09/396,196
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR PRICK FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR PRICK FILING DATE: 1998-09-17
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Matches 17; Conservative
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Matches 17; Conservative
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CORGANISM: mus musculus
US-10-809-189-92895
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; ORGANISM: Mus musculus
US-10-719-900-741411
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; ORGANISM: Mus musculus
US-10-719-900-841215
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US-10-719-900-841215/c
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LENGTH: 25
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Sequence 523845. Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3664.1

CURRENT PAPLICATION NUMBER: US/11/036,317

CURRENT PILING DATE: 2005-01-13

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOSTWARE: Microarray Probe Sequence Listing Generator V 1.1
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; Sequence 599645
; Sequence 599645, Application US/10719900
; Publication No. US2005026164A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; CURRENT APPLICATION NUMBER: US/10/719,900
; CRRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2003-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 599645
; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.3%; Score 15.2; DB 10; Length 25; 85.0%; Pred. No. 4.4e+03; tive 0; Mismatches 3; Indels o
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                                               3, Indels
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78.3%; Pred. No. 5.4e+03;
iive 0; Mismatches 5;
Score 15.2; DB 9;
Pred. No. 4.4e+03;
0; Mismatches 3;
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10S-10-809-189-57613/c
; Sequence 57613, Application US/10809189
; Publication No. US20050048531A1
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                                                                                             GATGCACAGCTGGGGAACAA 20
                                                                                                                       4 GCTGCAGAGCTGGGGAAGAA 23
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Matches 18; Conservative
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CORGANISM: Mus musculus
US-11-036-317-523845
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GENERAL INFORMATION:
FILE REPERENCE: 3527.1
FILE REPERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
FRIOR PRILING DATE: 2003-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 692355
LENGTH: 25
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Sequence 648791, Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:
TILLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REPERENCE: 3528.1

CURRENT FILING DATE: 2003-11-20

FRIOR PEDLICATION NUMBER: 60/427,808

FRIOR FILING DATE: 2002 11.20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.7%; Score 14.8; DB 7; Length 25; 88.9%; Pred. No. 6.7e+03; ive 0; Mismatches 2; Indels
                                                                                                                              Length 25;
                                                                                                                                                                       2; Indels
                                                                                                                       Score 14.8; DB 7;
Pred. No. 6.7e+03;
0; Mismatches 2;
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                                                                                                                            61.7%;
88.9%;
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                                           ; TYPE: DNA; ORGANISM: Rattus norvegicus
US-10-719-956-2771
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; ORGANISM: Rattus norvegicus
US-10-719-956-692355
                                                                                                                       Query Match
Best Local Similarity 88.9°
Matches 16, Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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Matches 16; Conservative
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; ORGANISM: Mus musculus
US-10-719-900-648791
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; SEQ ID NO 2771
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                      LENGTH:
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
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; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Vue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REPERRIENCE: 3527.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR APPLICATION NUMBER: 60/427,836
; RIJNG DATE: 2003-11-20
; PRIOR SEC ID NOTE: 2003-11-20
; NUMBER OF SEC ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.5%; Score 15; DB 9; Length 25; 78.3%; Pred. No. 5.4e+03; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15; DB 9; Lengtn 23, Pred. No. 5.48+03;
             APPLICANT: Michael Mittmann
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
FRIOR APPLICATION NUMBER: US/09/396,196
PRIOR APPLICATION NUMBER: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FRSEEQ for Windows Version 4.0
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Best Local Similarity 78.3<sup>3</sup>
Matches 18; Conservative
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CORGANISM: Probe Sequence
US-10-956-157-14605
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LENGTH: 25
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LENGTH: 25
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Sequence 198954, Application US/10719956

Sequence 198954, Application No. US20040146910A1

GENERAL INFORMATION:

SEQUENCE TO US20040146910A1

GENERAL INFORMATION:

TITLE OF INVENTION: Methods of Genetic Analysis of Rat

TITLE OF INVENTION NUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20

PRIOR FILING DATE: 2002-11-20

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25

LENGTH: 25
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; Sequence 58299, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: XUE Mel Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse; TITLE OF INVENTION: NUMBER: US/10/719,900
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT APPLICATION NUMBER: 60/427,808
; PRIOR PILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SEQ ID NO 58299
; LENGTH: 25
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81.0%; Pred. No. 8.3e+03;
tive 0; Mismatches 4;
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60.8%; Score 14.6; DB 8;
Best Local Similarity 81.0%; Pred. No. 9.3e+03;
Matches 17; Conservative 0; Mismatches 4;
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; SEQ ID NO 198953
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-198953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-198954
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US-10-719-900-58299/c
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                                          Sequence 315950, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Mounts, WILLE ALD ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SEQ ID NOS: 319805
SEQ ID NO 315950
LENGTH: 25
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Sequence 436639, Application US/11036317

Sequence 436639, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Williams, Alan

TILLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT FILING DATE: 2005-50-13

PRIOR PILING DATE: 2004-01-13

PRIOR PILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: You Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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; ORGANISM: Mus musculus
US-11-036-317-436639
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US-10-719-956-198953/c
                                US-10-956-157-315950/c
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APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Wounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WIT
TITLE OF INVENTION: HUMAN OSTEDARTHRITIS AND HUMAN PROTEASES
FILE REPERENCE: 031895-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILIAG DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 14606
LENGTH: 25
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US-11-036-317-81764

US-11-036-317

US-11-036-317

US-11-036-317

US-10-03-05-0214823A1

GENERAL INFORMATION:

APPLICANT: Blume, John

APPLICANT: Blume, John

CURRENT BLUMEN: John

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT PILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

WUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

ENAMENT: CONTRACT OF THE CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.8%; Score 14.6; DB 9; Length 25; Best Local Similarity 81.0%; Pred. No. 8.3e+03; Matches 17; Conservative 0; Mismatches 4; Indels
                                                                                                                                                              Length 25;
                                                                                                                                                          Score 14.6; DB 9;
Pred. No. 8.3e+03;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 14606, Application US/10956157; Publication No. US20050118625A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ATGCACAGCTGGGGAACAAGA 22
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                                                                                                                                                                                                                                                                                                                                                                       21 GATTCACACCTGAGAACAAG 1
                                                                                                                                                                 Query Match
Best Local Similarity 81.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-14606
                                ; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-14604
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LENGTH: 25
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TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
SUMMER OF SEQ ID NOS: 319805
SOFTWARE: PATENTIN VERSION 3.2
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; Sequence 267622, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse; TITLE OF INVENTION: Wethods of Genetic Analysis of Mouse; FILE REFERENCE: 3528.1
; CURRENT PAPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 267622
; LENGTH: 25
                                                     Sequence 267621, Application US/10719900

Publication No. US20050026164A1

GENERAL INPORMATION:

APPLICANT: Xue Mei Zhou

ITILE OF INVENTION: Methods of Genetic Analysis of Mouse;

FILE REFERENCE: 3528.1

FILE SPERIOR LATE: 2003-11-20

CURRENT APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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60.8%; Score 14.6; DB 8;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4;
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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US-10-719-900-267622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mus musculus
US-10-719-900-267621
                                   -10-719-900-267621/c
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NUMBER OF SEQ ID NOS: 991174
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US-11-016-317-552223

Sequence 552223, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

FRIDE NAPPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2005-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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| Sequence 770140, Application US/11036317
| Publication No. US20050214823A1
| Publication No. US20050214823A1
| GENERAL INFORMATION:
| APPLICANT: Williams, Alan
| APPLICANT: Williams, John
| TILLE OF INVENTION: Wethod of Analysis of Alternative Splicing in Mouse;
| FILE REPERENCE: 3654.1
| CURRENT APPLICATION NUMBER: US/11/036,317
| CURRENT FILING DATE: 2005-01-13
| PRIOR APPLICATION NUMBER: US 60/536,639
| PRIOR FILING DATE: 2004-01-13
                           US-11-036-317-189892/c
; Sequence 18982. Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
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                                                                                                                                                                                         FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 189892

LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14.6; DB 10;
Pred. No. 8.3e+03;
0; Mismatches 4;
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Best Local Similarity 81.0%;
Matches 17; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Mus musculus
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; ORGANISM: Mus musculus
US-11-036-317-552223
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Sequence 1997, Application US/10349143

Sequence 1997, Application No. US20040005584A1

Publication No. US20040005584A1

GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
TITLE OF INVENTION: Blainelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/10/349,143

CURRENT FILING DATE: 1999-10-20

PRIOR FILING DATE: 1999-10-20

PRIOR FILING DATE: 1999-10-20

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/109,732

PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-23

PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-23

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR SPLING DATE: EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NOS: 11796
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; Sequence 520335, Application US/10719900
; Suguence 520335, Application No. US2065026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OP INVENTION: Methods of Genetic Analysis of Mouse;
; TITLE OP INVENTION: WHERE: US/10/719,900
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 520335
                                                                                                                                                                                          Length 25;
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 770140 LENGTH: 25
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; LOCATION: 24
; OTHER INFORMATION: 99-7877-363 : polymorphic base A or
US-10-349-143-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 60.8%; Score 14.6; DB 6; 1
Best Local Similarity 73.9%; Pred. No. 8.2e+03;
Matches 17; Conservative 1; Mismatches 5;
                                                                                                                                                                                        60.8%; Score 14.6; DB 10;
81.0%; Pred. No. 8.3e+03;
ive 0; Mismatches 4;
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                                                                                                                                                                                                                                                17; Conservative
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ORGANISM: Homo Sapiens
                                                                                        TYPE: DNA
CORGANISM: Mus musculus
US-11-036-317-770140
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Matches 17; Conserv
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US-10-349-143-1997
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US-11-036-317-183105/c
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Job time : 661 secs
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Sequence 44464, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williama, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR PILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SEQ TEN NICROALTS Wicroarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 46464

LENGTH: 25
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
; AFPLICANT: Xue Mei Zhou
; TILE OF INVENTION:
; TILE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT APPLICATION NUMBER: 0503-11-20
; PRIOR APPLICATION UNDER: 600427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 520337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.0%; Score 14.4; DB 10; Length 25; Best Local Similarity 93.8%; Pred. No. 1e+04; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.0%; Score 14.4; DB 8; Length 25; 75.0%; Pred. No. 1e+04; tive 0; Mismatches 6; Indels
                                                                                     Query Match 60.0%; Score 14.4; DB 8; Length 25; Best Local Similarity 75.0%; Pred. No. 1e+04; Matches 18; Conservative 0; Mismatches 6; Indels
                                                                                                        1 GATGCACAGCTGGGGAACAAGACG 24
                                                                                                                                                                             1 GATGCACAGCTGGGGAACAAGACG 24
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Matches 18; Conservative
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CORGANISM: Mus musculus
US-11-036-317-46464
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; ORGANISM: Mus musculus
US-10-719-900-520337
                       ) ORGANISM: Mus musculus
US-10-719-900-520335
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  TYPE: DNA
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RESULT 39

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Sequence 271344, Application US/11036317
; Sequence 271344, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
    APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION: NUMBER: US/11/036,317
; CURRENT PILING DATE: 2005-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 271344
; LENGTH: 25
Sequence 183105, Application US/11036317
Sequence 183105, Application US/11036317
Substant Invogentation
APPLICANT: Williams, Alan
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT PILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 183105
LENGTH: 25
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Best Local Similarity 93.8
Matches 15; Conservative
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; ORGANISM: Mus musculus
US-11-036-317-271344
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COCANISM: Mus musculus
US-11-036-317-183105
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Sequence 32344, Ap
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Sequence 6394, Ap
Sequence 6784, Ap
Sequence 8469, Ap
Sequence 8469, Ap
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                                                                                                                                         December 13, 2005, 13:14:34 ; Search time 104.5 Seconds (without alignments) 408.244 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/PE_COMB.seq:*
/cgn2_6/ptodata/1/ina/PE_COMB.seq:*
/cgn2_6/ptodata/1/ina/PE_COMB.seq:*
/cgn2_6/ptodata/1/ina/PE_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-537-811-13

US-08-422-978-1997

US-09-422-978-1997

US-10-131-827-6696

US-10-131-827-6696

US-10-131-827-7086

US-09-422-978-1898

US-10-131-827-6784

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US-08-679-645-361
US-09-644-858-6
US-09-220-557-11
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US-09-396-1964-8421
US-09-396-1964-8421
US-09-396-1964-86727
US-09-33-33-317
US-09-033-428-18
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US-09-898-883-18
US-09-814-292-38
US-09-817-292-38
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18-00-316-196G-38995

18-00-316G-316G-316G-31895

18-00-316G-316G-31895

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Best Local Similarity 78.3%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 5;
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US-09-422-978-1997
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APPLICANT: CHO, JOONG MYUNG
APPLICANT: KIM, CHON HYUNG
APPLICANT: KIM, CHON HYUNG
APPLICANT: XIM, CHON HYUNG
APPLICANT: YANG, JAE YOUNG
APPLICANT: XIM, 10 SOO
APPLICANT: XIM, JOO HO
TITLE OF INVENTION: IMPROVED HCV DIAGNOSTIC
TITLE OF INVENTION: AGENTS
NUMBER OF SEQUENCES: 48
CONTRY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER: IBM COMPATION:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATION
DATE: 24-OCT-1995
CLASSIFICATION NUMBER: US/08/537,811
FILING DATE: 24-OCT-1995
CLASSIFICATION NUMBER: PCT/KR94/00040
FILING DATE: 29-APR-1993
ATTORNEY ABELICATION NUMBER: KR 93-7440
FILING DATE: 30-ARR-1993
ATTORNEY ABELICANTION NUMBER: KR 93-7440
FILING DATE: 30-ARR-1993
ATTORNEY ABELICANTION NUMBER: KR 93-7440
FILING DATE: 30-ARR-1993
ATTORNEY ABELICANTION NUMBER: MARKEN ABELICANTION NUMBER: MARK
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REFISENCE/DOCKET NUMBER: 8512-037-999
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-869-9741
TELEFAX: 212-869-9741
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
       NUMBER OF SEQ ID NOS: 127806
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 57613
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: primer PEIEGT2
US-08-537-811-13
                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ATGCACAGCTGGGGAACAAGACG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 ATGCAGAATAGGGAACAAGATG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/08537811
Patent No. 5910405
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                        ; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-57613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: Other
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US-08-537-811-13/c
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DB 2; Length 38;

62.5%; Score 15;

Query Match

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Sequence 1997, Application US/09422978

Sequence 1997, Application US/09422978

Bacture 1997, Application US/09422978

Bacture 1997, Application US/09422978

Bacture 1996, Application US/09422978

APPLICANT: Chumakov, Ilya

TILE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE GENEST.020CP1

CURRENT APPLICATION NUMBER: US/09/422,978

CURRENT FILING DATE: 1999-10-20

BARLIER APPLICATION NUMBER: US 09/298,850

BARLIER FILING DATE: 1999-04-21

BARLIER APPLICATION NUMBER: US 60/109,732

BARLIER FILING DATE: 1998-11-23

BARLIER FILING DATE: 1998-11-23

BARLIER FILING DATE: 1998-11-23

BARLIER FILING DATE: 1998-11-33

BARLIER FILING DATE: 1998-11-33

BARLIER PRILING DATE: 1998-11-33
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     Indels
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US-09-422-978-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-09-396-196G-103166
i Sequence 103166, Application US/09396196G
j Patent No. 6821724
i GENERAL INFORMATION:
APPLICANT: Michael Mittmann
j APPLICANT: David Mack
APPLICANT: David Lockhart
CURRENT SPLICATION WUMBER: 1050-10515
CURRENT APPLICATION WUMBER: 60/100,678
PRIOR PILING DATE: 1998-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 103166
LUNDE: LENGTH: 25
LUNDE: LENGTH: 25
LUNDE: APPLICATION
TOWNER: APPLICATION
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Best Local Similarity 73.9%; Pred. No. 1.8e+03;
Matches 17; Conservative 1; Mismatches 5;
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US-09-396-196G-103166
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ORGANISM: Homo Sapiens
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Sequence 1899, Application US/09422978
; Sequence 1809, Application US/09422978
; Fatent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Chamakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; TITLE OF INVENTION Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET. 020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; BARLIER FILING DATE: 1998-11-23
; NUMBER: OF SEQ ID NOS: 11796
; SEQ ID NO 1898
; SEQ ID NOS: 11796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
58.3%; Score 14; DB 3; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele; LOCATION: 24; OTHER INFORMATION: 99-718-261 : polymorphic base A or US-09-422-978-1898
                                                            3 TGCACAGCTGGGGAACAAGACG 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo Sapiens
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Sequence 7086, Application US/10131827

Patent No. 6905827

GENERAL INFORMATION:

APPLICANT: Woolgemuth, Jay

APPLICANT: Woolgemuth, Jay

APPLICANT: Woodward, Robert

TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

FILE REFERRENCE: 506612000120

CURRENT FILING DATE: 2002-09-06

PRIOR FILING DATE: 2001-06-08

PRIOR PLING DATE: 2001-06-08

NOFMBER OF SEQ ID NOS: 9090

SOFFWARE: Patent In version 3.1

SEQ ID NO 7086

LENGTH: SO
                                                                                                                                            Sequence 6696, Application US/10131827

Sequence 6696, Application US/10131827

Sequence 6696, Application US/10131827

GENERAL INFORMATION:

APPLICANT: Woodward, Robert

APPLICANT: Woodward, Robert

APPLICANT: Woodward, Robert

APPLICANT: Woodward, Robert

APPLICANT: Ly, NGOC

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

FILE REFERENCE: 506612000120

CURRENT PILING DATE: 2002-09-06

PRIOR APPLICATION NUMBER: US 60/296, 764

PRIOR PLING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 9090

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6996
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Pred. No. 2.9e+03;
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5 CACAGCTGGGGAACAAGAC 23
                                           5 cargecrerecaacaec 23
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Best Local Similarity 84.2%;
Matches 16; Conservative (
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Matches 16; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-10-131-827-6696
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APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERBENCE: AEOMYCA-7
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2001-01-30
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SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6666188
SEQ ID NO 8469
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88.2%; Pred. No. 3.8e+03;
tive 0; Mismatches 2; Indels
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patent No. 628463

GENERAL INFORMATION:
APPLICANT: Hasebe, Masahisa
APPLICANT: Goto, Masanisa
APPLICANT: Tosu, Mariko
ITLE OF INVENTION: Method for Detection of Mutations
FILE REFERENCE: PU96-1684
CURRENT PELLING DATE: 1999-08-18
PRIOR FILING DATE: 1999-08-18
PRIOR FILING DATE: 1999-08-18
PRIOR FILING DATE: 1996-06-29
PRIOR FLING DATE: 1996-06-29
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 5: LENGTH: 20
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         GU, Yizhong
JI, Yonggang
PENN, Sharron G.
HANZEL, David K.
RANK, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.2
Matches 15; Conservative
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Sequence 6784, Application US/10131827

Batent No. 6905827

GENERAL INFORMATION:

APPLICANT: Wooldward, Robert

APPLICANT: Wooldward, Robert

APPLICANT: Wooldward, Robert

APPLICANT: Wooldward, Robert

APPLICANT: Ly, NGW

TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

TITLE OF INVENTION: CHRONIC BAND

TITLE OF INVENTION WOMBER: US/10/106,290

PRIOR PLING DATE: 2001-02

PRIOR PLING DATE: 2001-06

NUMBER OF SEQ ID NOS: 9090

SOFTHARE: PATENTIN VETSION 3.1
Sequence 6394, Application US/10131827

Sequence 6394, Application US/10131827

GENERAL INFORMATION:

APPLICANT: Wohlgemuth, Jay

APPLICANT: Woodward, Robert

APPLICANT: Pry, Kirk

APPLICANT: Py, May

APPLICANT: Woodward, Robert

APPLICANT: Py, May

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

FILE REFREENCE: 50661200120

CURRENT FILING DATE: 2002-09-06

PRIOR PILING DATE: 2001-06-08

PRIOR PILING DATE: 2001-06-08

PRIOR FILING DATE: 2001-06-08

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6394

LENGTH: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 58.3%; Score 14; DB 3; Length 50; Best Local Similarity 100.0%; Pred. No. 3.5e+03; Matches 14; Conservative 0; Mismatches 0; Indels
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Sequence 8469, Application US/09866108A
Patent No. 6686188
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Best Local Similarity 100.
Matches 14; Conservative
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US-10-131-827-6784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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LENGTH: 50
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Gaps

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APPLICANT: CHEN, WEAR MEASON, MARK

APPLICANT: SHANKON, MARK

TITLE OF INVENTION: WOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEGAMICA-7

CURRENT APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PLING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR APPLICATION NUMBER: PCT
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APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: BENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David R.
APPLICANT: HANZEL, David R.
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: WROSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: AEGOMICA-7
CURRENT APPLICATION NUMBER: US 60/207,456
FRICH APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-77
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.5%; Score 13.8; DB 3;
88.2%; Pred. No. 4e+03;
live 0; Mismatches 2;
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; Sequence 13363, Application US/09866108A
; Patent No. 6686188
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-866-108A-13362
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-105-26
PRIOR PILING DATE: 2000-105-26
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
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                                                                          57.5%; Score 13.8; DB 3; Length 20; 88.2%; Pred. No. 3.9e+03; ive 0; Mismatches 2; Indels
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88.2%; Pred. No. 4e+03;
tive 0; Mismatches 2;
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Patent No. 6686188
SEQ ID NO 13361
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; Sequence 13361, Application US/09866108A
; Patent No. 6686188
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: RANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wenbheng
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Best Local Similarity 88.2<sup>3</sup>
Matches 15; Conservative
                                                                                                                                                            Conservative
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                                                                          Query Match
Best Local Similarity
Matches 15; Conserv
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US-09-194-478-5
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Length 25; Indels

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; ORGANISM: Homo sapiens
US-09-866-108A-13364
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APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
ITILE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE FILE REFERENCE: AEOMICA-5-25
CURRENT FILING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-00-27
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PAPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING BATE: 2001-01-30
PRIOR PILING BATE: 2001-01-30
PRIOR PILING BATE: 2001-01-30
PRIOR PILING APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 13364
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Pred. No. 4e
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Patent No. 6686189
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
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Best Local Similarity 88.2%;
Matches 15; Conservative
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CORGANISM: Homo sapiens
US-09-866-108A-13363
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; DB 3; Length 25;
4e+03;
                 Indels
Query Match 57.5%; Score 13.8; E
Best Local Similarity 88.2%; Pred. No. 4e+(
Matches 15; Conservative 0; Mismatches
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; Sequence 13366, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AGCTGGGGAACAAGACG 24
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                                  8 AGCTGGGGAACAAGACG 24
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                                                                           RESULT 18
US-09-866-108A-13365
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APPLICANT: RANK, David R.

PRELICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR OF ILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR OF ILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.5%; Score 13.8; DB 3; Length 25; 88.2%; Pred. No. 4e+03;
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PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13368, Application US/09866108A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 15; Conserv
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US-09-866-108A-13368
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                                                                                            APPLICANT: HANKEL, David R.
APPLICANT: HANKEL, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
TITLE OF INTERIOR TO THE WOOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ACMICA-7
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/206,359
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2001-01-30
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APPLICANT: DENN, Sharron G.
APPLICANT: PENN, Sharron G.
APPLICANT: PENN, Sharron G.
APPLICANT: RANKEL, David K.
APPLICANT: RANKEL, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, WASIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AROMICA-1
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 6236,535
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-10-03
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NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6866188
SEQ ID NO 13366
LENGTH: 25
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Pred. No. 4e+03;
^. Wismatches 2; Indels
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Patent No. 6686188
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Best Local Similarity 88.2%;
Matches 15; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-866-108A-13366
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US-09-866-108A-13367
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RESULT 25
US-09-101-927-5
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US.09-866.108A-13869
US.09-866.108A-13869
EQUERAL NO. 6666.108
EQUERAL INCORMITON:
APPLICANT: INCORMITON:
APPLICANT: PENN, STARTON G.
APPLICANT: PENN, STARTON G.
APPLICANT: PENN, STARTON G.
APPLICANT: ARNE, David R.
APPLICANT: ARNE, David R.
APPLICANT: ARNE, David R.
APPLICANT: ARNE, David R.
APPLICANT: SHANNON, MARK
ITITE OF INVENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE FILE REFERENCE: ASONICA-7
CURRENT FILING DATE: 2000-52-5
FRIOR APPLICATION NUMBER: US 60/207,456
FRIOR APPLICATION NUMBER: US 60/207,456
FRIOR APPLICATION NUMBER: US 60/206,556
FRIOR APPLICATION NUMBER: BCT/US01/0066
FRIOR PRILING DATE: 2000-10-04
FRIOR APPLICATION NUMBER: PCT/US01/0066
FRIOR PRILING DATE: 2001-01-30
FRIOR PRILING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
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                                                                                                                                                              Gaps
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                                                                                                  Score 13.8; DB 3; Length 25;
Pred. No. 4e+03;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Acomica Sequence Listing Engine
Patent No. 1686188
SEQ ID NO.13369
LENGTH: 25
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                                                                                                        Query Match
Best Local Similarity 88.2%;
Matches 15; Conservative
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US-09-866-108A-13369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13368
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Sequence 3653, Application US/09422978 Patent No. 6537751 GENERAL INFORMATION:

US-09-422-978-3853/c

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APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Billic markers for use in constructing a high density...
FILE REPERENCE: GENSET.020cP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 3853
LENGTH: 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: 99-3608-264 : polymorphic base A or US-09-422-978-3853
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; Sequence 57614, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION.
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE NETERENCE: 3101.1
; CURRENT APPLICATION UNDER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR REPLING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOSTWARE: FREEEN FOR MINDORE 127806
; SOSTWARE: FREEEN FOR MINDORE 127806
; SOSTWARE: FREEEN FOR MINDORE 127806
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80.0%; Pred. No. 4.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.8; DB 3;
Pred. No. 4.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ATGCACAGCTGGGAACAAG 21
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78.9%;
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Best Local Similarity 78.9°
Matches 15; Conservative
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CORGANISM: mus musculus
US-09-396-196G-57614
                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo Sapiens
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Best Local Similarity
Matches 16; Conserva'
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LENGTH: 25
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US-09-64-4858-6

US-09-644-858-6

Sequence 6, Application US/09644858

Patent No. 6933364

GENERAL INFORMATION:

APPLICANT: Tosho Corporation

APPLICANT: Hattori, Yoshiyuki

APPLICANT: Hattori, Toshiyuki

APPLICANT: Hattori, Toshiyuki

TITLE OF INVENTION: SECRETORY THYROID STIMULATING HORMONE RECEPTOR, AND METHOD FOR

TITLE OF INVENTION: ANTI-THYROID STIMULATING HORMONE RECEPTOR ANTIBODY USING THE SI

FILE REFERENCE: PA21-046

CURRENT APPLICATION UNDER: US/09/644,858

CURRENT FILING DATE: 205

NUMBER OF SEQ ID NOS: 25

SOSTWARE: Patentin version 3.0
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56.7%; Score 13.6; DB 3; Length 34;

Best Local Similarity 80.0%; Pred. No. 5.1e+03;

Matches 16; Conservative 0; Mismatches 4; Indels
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                          LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The letter "N" stands for any base.
                                                                                                                                                                                                                                                                              5; Indels
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Sequence 11, Application US/09220557A

Patent No. 6515206

GENERAL INPORMATION:
APPLICANT: Chaudhuri, Sumita
TITLE OF INVENTION: PLASTID TRANSFORMATION OF BRASSICA

FILE REPRENCE: 15398/00/US

CURRENT APPLICATION NUMBER: US/09/220,557A

CURRENT FILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 19

SEQ ID NO 11

LENGTH: 49
                                                                                                                                                                                                                          Score 13.6; DB 3;
Pred. No. 5.1e+03;
2; Mismatches 5;
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; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-220-557-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
| LOCATION: ()...()
| OTHER INFORMATION: sense primer shTSHR-2
| OS-09-644-858-6
                                                                                                                                                                                                                                                                                                                                1 GATGCACAGCTGGGGAACAAG 21
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                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial/Unknown
     SEQUENCE CHARACTERISTICS
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US-09-220-557-11/c
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LENGTH: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zwick, Michael G.
APPLICANT: Zwick, Michael G.
APPLICANT: Bedington, Brent E.
APPLICANT: McSwiggen, James A.
APPLICANT: Mcrlo, Parricia Ann Owens
APPLICANT: Guo, Lining
APPLICANT: Young, Scott A.
APPLICANT: Young, Scott A.
APPLICANT: Polkerts, Otto
APPLICANT: Polkerts, Otto
APPLICANT: Mcrlo, Donald J.
TITLE OF INVENTION: COMPOSITION OF GENE EXPRESSION
TITLE OF INVENTION: IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
ADDRESSEE: Lyon & Lyon
CURRENT APPLICATION NUMBER: US/09/101,927
CURRENT FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: PGT/US97/026735
EARLIER APPLICATION NUMBER: 60/012,218
EARLIER APPLICATION NUMBER: 60/012,218
EARLIER APPLICATION NUMBER: 60/012,218
EARLIER PILING DATE: 1996-02-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Lyon & Lyon
STREET: 613 Weet Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM COMPACTION
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,645
FILING DATE: U3/12,1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 06/001,135
FILING DATE: U11y 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: SEPTEMBER: 08/300,726
FILING DATE: SEPTEMBER: 08/300,726
ATTORNEY/AGENT INFORMATION:
NAME: WAADDURG, RICHARD J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 361, Application US/08679645
Patent No. 6350934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GATGCACAGCTGGGGAACAA 20
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INFORMATION FOR SEQ ID NO: 361:
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                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-101-927-5
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Gaps
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US-09-396-196G-107466/C
Sequence 107466, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mackhart
APPLICANT: David Lockhart
TILE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FRatLSEQ for Windows Version 4.0
SEQ ID NO 107466
LANDER OF THE SECOND OF THE SEQ OF THE SECOND O
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Pred. No. 6.1e+03;
0; Mismatches 6;
                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.4; DB 3;
Pred. No. 6.1e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 95727
LENGTH: 25
                                                                                                    ; Sequence 95727, Application US/09396196G; Patent No. 6821724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 ATTCACAGCTGTTTAAAAAGAGG 3
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Patent No. 6197293;
GENERAL INFORMATION:
APPLICANT: Yu, De Chao
APPLICANT: Schuur, Eric
APPLICANT: Henderson, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.8%;
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93.3%;
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Best Local Similarity 73.99
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: mus musculus
US-09-396-196G-95727
                                                                            US-09-396-196G-95727
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US-09-033-333-17/c
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                                            Gaps
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Pred. No. 6.1e+03;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 49;
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                                            Indels
                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/10219227

Patent No. 6891086

GENERAL INFORMATION:
APPLICANT: Oakes, Janette V.
APPLICANT: Oaken, Janette V.
TILE OF INVENTION: PLASTID TRANSFORMATION OF BRASSICA
FILE REFERENCE: 15398/01/US
FURRENT APPLICATION NUMBER: US/10/219,227
CURRENT FILING DATE: 2002-08-15
PRIOR FILING DATE: 1999-12-17
PRIOR PLICATION NUMBER: US/09/465,856
PRIOR APPLICATION NUMBER: US/09/465,856
PRIOR APPLICATION NUMBER: US/09/220,557
PRIOR PLING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 30
US-09-196G-88421
i Sequence 84421, Application US/09396196G
i Patent No. 6821724
i GENERAL INFORMATION:
APPLICANT: Mitcheal Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
ITILE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FREASEQ for Windows Version 4.0
SEQ ID NO 88421
LENGTH: 25
    80.0%; Pred. No. 5.4e+03;
tive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 56.7%; Score 13.6; DB 3; Best Local Similarity 80.0%; Pred. No. 5.4e+03; Matches 16; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
FRATURE:
// OTHER INFORMATION: Synthetic Oligonucleotide
US-10-219-227-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Argcgcrcrrgggaacaarcg 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 CACAGCTGGGGAACAAGACG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 CACAGCGAGGAGCAAGTCG 20
                                                                                                                        5 CACAGCTGGGGAACAAGACG 24
                                                                                                                                                                                                 39 CACAGCGAGGGAGCAAGTCG 20
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Best Local Similarity 73.9%;
Matches 17; Conservative
                                            16; Conservative
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-396-196G-88421
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US-10-219-227-11/c
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D
                                            Matches
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APPLICANT: Henderson, Daniel R.
APPLICANT: Yu, De Chao
TITLE OF INVENTION: ADENOVIRUS VECTORS CONTAINING
TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
TITLE OF INVENTION: OF USING SAME
TITLE OF INVENTION: OF USING SAME
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
CITY: Palo Alto
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.8%; Score 13.4; DB 3; Length 30; 73.9%; Pred. No. 6.3e+03; ive 0; Mismatches 6; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COPERATING SYSTEM: Windows

COPERATING SYSTEM: Windows

SOFTWARE: FastSEQ for Windows

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/033,556

FILING DATE:

CLASSIFICATION NUMBER:

FILING APPLICATION

APPLICATION NUMBER:

FILING DATE:

ATTORNEY AGENT INFORMATION:

NAME: Catherine, Polizzi M

REGISTRATION NUMBER: 40,130

REFREENCHOUSING NUMBER: 34802-20010.00

TELEPHONE: 650-811-5600
                                                                        ATTORNEY/AGENT INFORMATION:
NAME: POLIZZI, CATHERINE M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-30004.00
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 813-5600
TELEFAX: (415) 814-0792
TELEFAX: (415) 816-0792
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: NUCLEIC acid
TYPE: NUCLEIC acid
TYPE: NUCLEIC acid
TYPE: NUCLEIC acid
       APPLICATION NUMBER: US/09/033,428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ATGCACAGCTGGGGAACAAGACG 24
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Patent No. 6432700
GENERAL INFORMATION:
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TELEX: 706141
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS: LENGTH: 30 base pairs;
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-033-556-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 73.99
Marches 17; Conservative
                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-033-556-40/c
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          ADENOVIRUS VECTORS SPECIFIC
FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-033-428-18/c

Sequence 18, Application US/09033428

Sequence 18, Application US/09033428

Patent No. 6254862

GENERAL INFORMATION:
APPLICANT: Little, Andrew
APPLICANT: Little, Andrew
APPLICANT: Schuur, Eric
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGE TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGE NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS: 22 CORRESPONDENCE ADDRESS: ADDRESSE: MORRISON & FOERSTER STATE: CATOLINE NEAD ALCO STATE: CATOLINE READABLE FORM: MEDIUM TYES DISKETTE OF COMPUTER: IBM Compatible COMPUTER: IBM Compatible OPERATING SYSTEM: Windows Version 2.0b SOFTWARE: Fast-SEQ for Windows Version 2.0b CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION SECONDENCE OF MENONES SOFTWARE FILING DATE: FILING DATE: FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: 40.130 REFERENCE/DOCKET NUMBER: 34802-20007.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ATGCACAGCTGGGGAACAAGACG 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , TOPOLOGY: linear
US-09-033-333-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
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Gaps . 0

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Schuur, Eric
Henderson, Daniel
TITLE OF INVENTION: ADBNOVIRUS VECTORS SPECIFIC FOR CELLS
EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 30;
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Sequence 6, Application US/08462159B

Patent No. 6787640

GENERAL INFORMATION:
APPLICANT: Greene Ph.D., John M.
APPLICANT: Dillon Ph.D., Patrick J.
TITLE OF INVENTION: Fibroblast Growth Factor 14
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Grewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,883
FILING DATE: 02-011-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/033,428
FILING DATE: cUnknown>
ATTORNEY/AGENT INFORMATION:
NAME: POLIZZI, CATHERINE M.
REGISTRATION NUMBER: 40,130
REGISTRATION NUMBER: 34802-30004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 813-5600
TELEFAX: (415) 813-5600
TELEFAX: (415) 819-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 73.9%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ATGCACAGCTGGGGAACAAGACG 24
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 AAGCAGAGGGTGGAACAAAGG 3
Lamparski, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                            SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WordPerfect 5
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ZIP: 07068-1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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55.8%; Score 13.4; DB 3; Length 30;
Best Local Similarity 73.9%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels
                     55.8%; Score 13.4; DB 3; Length 30; 73.9%; Pred. No. 6.3e+03; Live 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Catherine, Polizzi M
REGIGSTRATION UNDRER: 460.130
REFERENCE/DOCKET UNDRER: 34802-20007.00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/614,495
FILING DATE: 11-Jul-2000
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
PRIOR APPLICATION WUNBER: 09/033,333
PILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                      2 ATGCACAGCTGGGGAACAAGACG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 AAGCAGAGCGGTGGAACAAAGG 3
                                                                                                                                                                    25 AAGCAGAGCGGTGGAACAAAGG 3
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; Sequence 18, Application US/09898883
; Patent No. 6885968
; GENERAL INFORMATION:
; APPLICANT: Little, Andrew
                                                                                                                                                                                                                                                                              Sequence 17, Application US/09614495
Patent No. 6436394
GENERAL INFORMATION:
APPLICANT: Yu, De Chao
Schuur, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                        Query Match
Best Local Similarity 73.99
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: CA
                                                                                                                                                                                                                                        RESULT 36
US-09-614-495-17/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-614-495-17
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TYPE: DNA
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gequence 38, Application US/09814292

gequence 38, Application US/09814292

gequence 38, Application US/09814292

general No. 6852528

general No. 685201500

general No. 685200

general No. 68520

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 55.8%; Score 13.4; DB 3; Length 30; Best Local Similarity 73.9%; Pred. No. 6.3e+03; Matches 17; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.8%; Score 13.4; DB 3; Length 30; 73.9%; Pred. No. 6.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                             APPLICATION NUMBER: US/08/462,159B
PILING DATE: 05-JUN-1995
CLASSIPICATION: 435
CLASSIPICATION ATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/207,412
FILING DATE: 08-MAR-1994
ATTOWNAME: MARL-1994
ATTOWNAME: MARL-1994
ATTOWNAME: MARR-1994
REGISTRATION NUMBER: 33,073
REGISTRATION NUMBER: 325800-440
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                       325800-440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: PCR Primer 37.124.3
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US-09-875-228-24/c
'Sequence 24, Application US/09875228
'Patent No. 6916918
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 73.9
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-814-292-38/C
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APPLICANT: Henderson, D.R.
APPLICANT: Honderson, D.R.
TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE
TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE
FILE REFERENCE: 348022000300
CURRENT APPLICATION NUMBER: US/09/875,228
CURRENT APPLICATION NUMBER: 09/127,834
PRIOR PLING DATE: 1996-08-03
PRIOR FILING DATE: 1996-08-03
PRIOR FILING DATE: 1996-08-03
PRIOR FILING DATE: 1996-08-04
PRIOR FILING DATE: 1996-08-04
PRIOR FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIAL OF SEQ ID NOS: 38
SOFTWARE: PATENTIAL OF SEQ ID NOS: 38
SOFTWARE: PATENTIAL OF SEQUENCE
PRACTICE: 0916-08-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIAL SEQUENCE
PRACTICE: 0916-08-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIAL OF SECUENCE SYNTHETICALLY
ORGANISM: Artificial Sequence
PRACTICE: 0916-08-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: 100-04
NUMBER OF SEQ ID NOS: 18:55:00
SCANDISM: 100-04
NUMBER OF SEQ ID NOS: 18:55:00
USCANDISM: 100-04
NUMBER OF SEQ ID NOS: 18:55:00
USCANDISM: 100-04
NUMBER OF SEQ ID NOS: 18:55:00
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CW986355 KBrH012L0

AZ814914 2M0082C24 BH655497 SALK 0850 BH656386 100713H0 BH640991 1008039E0 CZ469449 C04702-3p BM395302 50072-2-8 AA776443 zj50h10.8 AA739879 AJ239879 AA239879 AJ239879 AA25767 AV255694 AJ792767 AJ792767 AI254367 QV33310.x AI254367 QV33310.x AI2566 AU105506 AU105506 AU105506

C2909855 4018011H1 DN955268 it84h05.9 R10392 yf37e03.81 CC798667 SALK 1472 CC798676 SALK 1472 AZ501408 1M0340E13

AG199766 Pan trod

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ROSAbetageo+1 gene trap. Sequence tag generated by 5'RACE.
Additional sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result clone.html?
clone id=WSSESB01' Es cell line harboring insertion mutation of
target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.html'
l'Inhouse Sequence Identifier: 12462
                                                                                                                                                                                                                                                                                                                                                                                                                                     JS DP MRNA linear GSS 22-MAR-2005 W255E01 GGTC Gene Trap Library GV04C04 Mus musculus cDNA clone W255E01, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murcidea; Murinae; Mus.

1 (bases 1 to 38)
Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F., Arnold,H.H., Schnutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P. A large-scale; gene-driven mutagenesis approach for the functional analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Jan 27, 2005 this sequence version replaced gi:40731354
Contact: GGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Embryonic stem cell"
/cell_line="ES cells 12952 (formerly 129/SvPas)"
/clone_lib="GGTC Gene Trap Library GV04C04"
/note="Vector: ROSAbetageo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .38
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="W255E01"
                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: GGTC
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
                                                                                                               AJ239879
AA287473
AUS55694
AJ792767
ALZ54367
ALZ54367
AU105507
CZ909855
                                                                                                                                                                                                                                                                                                         AZ501408
AG199766
                                                                      CZ469449
                                                                                                                                                                                                                                               DN955268
                                          BH626386
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                                                                                                                                                                                                                                                                                           CC798676
                                                                                     BM395302
                                                                                                   AA776443
                                                        BH640991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CL214453.2 GI:49489711
                                          910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex="Male"
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VERSION
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COMMENT
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CL214453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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CR396399 Arabidops
AL945338 Arabidops
AU103763 AU103763
AZ769231 1M0569607
AI156750 ue54b07.r
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AZ511249 1M0356N10
AA958372 ualla03.r
                                                                                                 ; Search time 2984 Seconds (without alignments) 376.304 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
               GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                              41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                    December 13, 2005, 12:51:49
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AZ769231
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AU103768
AU104109
AZS65607
BH865278
AV822547
AG200388
CZ472331
                                                                      - nucleic search, using sw model
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Match Length DB
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9b e8t2: *
9b btc: 3 *
9b htc: 3 *
9b e8t4: *
9b e8t7: *
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                              Copyright
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Maximum DB seq length: 50
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/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weisshaar, --,.., college, netss, b., bekker, k. and Meisshaar, B. An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for Elanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                     CR396399 46 bp DNA linear GSS 01-MAY-2004
Arabidopsis thaliana T-DNA flanking sequence GK-198G05-025984,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
bukaryota, Viridplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_zref="taxon:3702"
/clone="GK-198005-025984"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database the identification of T-DNA insertion mutants in Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
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                         60.8%; Score 14.6; DB 9; Length 37; 81.0%; Pred. No. 7.9e+04; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bioinformatics 19 (11), 1441-1442 (2003)
12874060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic survey sequence
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                                                                                                    17; Conservative
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                                                                   Best Local Similarity
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                                                                                                    Matchee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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/ clone lib="Mouse 10kb plasmid UUGCIM library"
/ clone lib="Mouse 10kb plasmid UUGCIM library"
/ clone lib="Mouse 10kb plasmid UUGCIM library"
/ note="Weetor: PWD42nv; Purified genomic DNA from M."

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
/ (http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored NNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|RR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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2M0112P10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0112P10 R, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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   Length 38;
Query Match 62.5%; Score 15; DB 10; Length 38
Best Local Similarity 78.3%; Pred. No. 5.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels
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Fax: 801 585 7177
Email: ddunn@genet.cs.utah.edu
Insert Length: 10000 Std Error: 0.(
Plate: 0112 row: P column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0112P10"
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Location/Qualifiers
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                                                                                                                                                                                                           7 ATTTAGAGCTGCGGAACAGGACG 29
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                                                                                                                                           2 ATGCACAGCTGGGGAACAAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ832358.1 GI:13002266
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84112, USA
                                                                                                                                                                                                                                                                                                                   RESULT 2
AZ832358/c
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19 bp DNA linear GSS 16-FEB-2001 1M0569G07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0569G07 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                             AU103763 Sugano Homo sapiens cDNA linear EST 28-JAN-2004 AU103763 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HEP10745, mRNA sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae, Homo.

Hominidae, Homo.

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Bata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Biverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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/db_xref="taxon:9606"
/clone="HEP10745"
/clone=lib="Sugano Homo sapiens cDNA library"
                                      Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.3%; Score 14; DB 1; Length 50; 77.3%; Pred. No. 1.5e+05; rive 0; Mismatches 5; Indels
                                                                                     5; Indels
                                      Score 14; DB 10;
Pred. No. 1.5e+05;
                                                                                     0; Mismatches
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                                                                                                                                 1 GATGCACAGCTGGGGAACAAGA 22
                                                                                                                                                              Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yutaka Suzuki
                                         58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Conservative
                                                                                       17; Conservative
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Matches 17; Conserv
                                           Query Match
Best Local Similarity
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Direct Submission

Submitted (31-MR-2004) Weisshaar B., Max-Planck-Institut fuer
Submitted (31-MR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
FSD14. Details on the protocols used for generation of the sequence
are described in References 1-3. The sequences are generated at the
MPI for Plant Breeding Research in the context of the GABI-Kat
project GABI-Kat is part of the German Plant Genomics program
designated 'GABI- Information on line availability can be found
at: http://www.mpiz-koeln.mapg.de/GABI-Rat/.
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/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAc161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment (s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
An Axabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for Flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
                                                                                                                                                                                                                                                                                                  AL945338 10-APR-2004 Sequence GK-288F04-015346,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
BioTechniques 35 (6), 1164-1168 (2003)
                                                                                            Gaps
                                                                                            ö
                                           Score 14.6; DB 11; Length 46;
Pred. No. 8e+04;
0; Mismatches 4; Indels C
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12874060
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/db_xref="taxon:3702"
                                                                                                                                          2 ATGCACAGCTGGGGAACAAGA 22
                                                                                                                                                                                      45 acccacacacacacaaaaaa 25
                                                                                                                                                                                                                                                                                                                                                            genomic survey sequence
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                                                60.8%;
81.0%;
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                                                                                               17; Conservative
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       ORIGIN
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CL844510

EX12606-5prime Drosophila melanogaster P{EPgy2} P element insertion lines Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey sequence.
                                     (bases 1 to 31)
Marrah., Hillar,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Marrah., Hillar,L., Allen,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="Scares mammary gland NMLMG"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(HT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

E 1 (Dases 1 to 38)
E 2 (Dases 1 to 38)
E 3 (Dases 1 to 38)
E 4 (2011)
E 5 (Dases 1 to 38)
E 6 (2011)
E 7 (Dases 1 to 38)
E 7 (Dases 1 to 38)
E 7 (Dases 1 to 38)
E 8 (Dases 1 to 38)
E 9 (Dases 1 to 38)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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   Sciurognathi; Muroidea; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.0%; Score 13.2; DB 1;
83.3%; Pred. No. 3.4e+05;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="INAGE:1494901"
/ciseue_type="mammary gland"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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Matches 15; Conservative
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CL844510/c
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AII56750 AII56750.1 GI:3685219
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Nus musculus
Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Neselly, M., Rose, M., Rose, R., Stoken, R., Tingey, A., von Niederhausern, A. and Wright, D., Walse, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, 184112, USA.
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Ilsert Length: 10000 Std Error: 0.00
Plate: 0569 row: G column: 07
Seg primer: CACACAGGAAACAGCTAATGACC
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/strain="C57BL/6J"
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/clone="UUGC1M0569G07"
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Location/Qualifiers
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                                                                                                                                                                 The P element insertion position is base 31 in the 38 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Inverse PCR was performed on Drosophila melanogaster strains each of which contains one or more P{EPgy2} P-element transposon insertion. The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://www.fruitfly.org/about/methods/inverse.pcr.html."
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Dunn, D., Aoyagi, A., Barber, M., Reacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: S106439947
Email: gerry@fruitly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
                                                                                                                                                                                                                                                                                                                 /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone libe="Drosophila melanogaster P{EPgy2} P element
insertion lines"
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Insert Length: 10000 Std Error: 0.00
Plate: 0284 row: H column: 11
Seg primer: CACAAAGGAAACAGCTAATGACC
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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High quality sequence stop: 41.
Location/Qualifiers
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Location/Qualifiers
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymcleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pMAP2 (gql 4732114)[gbl AP129072.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 43)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                        /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note=""Vector: PWP42nv; Purified genomic DNA from M. musculus C57BL/63 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/db_xref="taxon:9606"
/clone="IMAGB:174300"
/dev stage="19 weeks"
/lab_host="blide"
/clone_lib="Soares_fetal_lung_NbHL19W"
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/db_xref="taxon:10090"
/clone="UUGC1M0284H11"
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AI185696.1 GI:3736334
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                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 76.29
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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Hef-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshiromo-Dakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU104109 AUGAIN SUGAIN HOMO BADIENS CDNA LIDEAR EST 28-JAN-2004 AU104109 Sugano Homo Bapiens cDNA Library Homo Bapiens CDNA Clone HEP13777, mRNA sequence.
                                                                                                                                                                                                                                                                              AU103768 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HEP12651, mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae, Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakati, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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/clone_lib="Sugano Homo sapiens cDNA library"
                                           Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.2%; Score 13; DB 1; Length 50; 76.2%; Pred. No. 4.4e+05; 1.ve 0; Mismatches 5; Indels
                                  Score 13; DB 10; Li
Pred. No. 4.3e+05;
n: Mismatches 5;
                        54.2%; Scor.
76.2%; Pred. No. 4...
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/mol_type="mRNA"
/db_xref="taxon:9606"
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AU104109.1 GI:13553630
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Best Local Similarity 76.2<sup>3</sup>
Matches 16; Conservative
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1 (bases 1 to 50)
                                                                                        16; Conservative
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Matches 16; Conserv
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/mol_type="genomic DNA"
/culfivar="mixed background W23/A188/B73"
/tisenulxed background W23/A188/B73"
/tisenue_type="leaf"
/tev stage="leaf"
/dev stage="leaf"
/dev stage="leaf"
/dev stage="leaf"
/dev stage="leaf"
/dev stage="langle"
/clonellb="ll18 - RescueMu (engineered from note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi, Site 2: BglIi;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu. Grid & was grown at San Diego in 2002. DNA was
extracted from leaf strips, double digested using BamHi
and BglII, and ligated to form circular plasmids. DH108
cells were transformed and then screened on LB plates with
ampicillin."
1118044H12.2EL_y1 1118 - RescueMu Grid S Zea mays genomic, genomic CG803673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 43)
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Fax: 650 725 8221
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/organism="Zea mays"
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                                                                                                                                                                                                                                                                                                                                                           16; Conservative
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Zea mays
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/dev stage="asexual blood forms"
/dab_nost="saimiri boliviensis"
/dab_nost="saimiri boliviensis"
/clone lib="Pw MBN #16 (amplified twice)"
/note="Vector: Lambda ZAP II (Stratagene); individual
/note="vector: Lambda ZAP II (Stratagene); individual
/notes excised into phagemid pBluescript; Site 1: EcoR I;
Site 2: EcoR I; Genomic DNA was prepared from asynchronous
blood stage forms of the Belem line of P. vivax grown in
squirrel monkeys. Parasitized erythrocytes were purified
                                                                                                                                                      Department of Virology
Institute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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211PvA09 Pv MBN #16 (amplified twice) Plasmodium vivax genomic 3',
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
BENDO Rep. 2 (5), 388-393 (2001)
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 50)

Carlton,J.M.-R. and Dame,J.B.

The Plasmodium vivax and P. berghei gene sequence tag projects
Parasitol. Today 16 (10), 409 (2000)
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Dept. of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
Tel: 352 392 4700
Fax: 352 392 9704
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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="taxon:9606"
/clone="HEP13777"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 50;
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Pred. No. 4.4e+05;
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/organism="Plasmodium vivax"
/mol type="genomic DNA"
/strain="Belem"
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Seg primer: M13(-20) forward
Class: shotgun.
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from contaminating host leukocytes by filtration of ADP activated blood through acid-washed glass beads and Whatman CF11 cellulose columns by gravity filtration. Purified DNA was digested with mung bean nuclease in the presence of 42.5% formanide at 500C as described (Galinski, M. et al. 1992. Cell 69,1213-1226; Vernick, K.D. et al.1988. N.A.R. 16, 6881-6896). Eco RI linkers were added and the constructs ligated into Lambda ZAP II. P. vivax Belem was originally isolated from a patient in Belem, Brazil 1980 by Mercia de Arruda, adapted to Saimiri monkeys by Jurg Gysin, and maintained since 1983 in squirrel monkeys."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH865278 1inear GSS 05-AUG-2002 SALK 098078 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_098078, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
1 (bases 1 to 42)
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A Sequence-Indexed Library of Insertion Mutations in the
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Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
This 85 453 4100 A.7752
Eax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of This is sequence lies within an annotated exon of At3g23970.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.2%; Score 13; DB 9; Length 50; 76.2%; Pred. No. 4.4e+05;
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/mol type="genomic DNA"
/ecotype="Col-0"
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Best Local Similarity
Matches 17; Conserv
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Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Roptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Rophydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

(bases 1 to 43)

Et (bases 1 to 43)

Et
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H. Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea (GRC); (B-mail:redetoneemail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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d01604-3prime Exelixis P element XP insertions Drosophila
melanogaster genomic Sequence recovered from 3' end of P element,
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Berkeley Drosophila Genome Project
Berkeley Nososphila Genome Project
Lawrence Berkeley, National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
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The P element insertion position is 1 in the 43 bases. This
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/clone_lib="RP-43 Chimpanzee Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 30;
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-082F17.T7"
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LIBRARY
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R.Site 1
R.Site 2
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CZ472331/c
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PUBMED
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AUTHORS
                                                                    TITLE
JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                         AV832547 K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare leaves vegetative stage Hordeum vulgare gubsp. clone baak12a18, mRNA sequence.
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Pan troglodytes DNA, clone: RP43-082F17.T7, genomic survey
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Hordeum vulgare subsp. vulgare
Bukaryota, Viridiplantea, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooldeae, Triticeae, Hordeum.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="baak12a18"
/tissue type="leaves"
/dev_atage="vegetative stage"
/clone lib="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare leaves vegetative stage"
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/cultivar="Akashinriki"
/sub_species="vulgare"
/db_xref="taxon:112509"
                                                                            GATGCACAGCTGGGGAACAAGACG 24
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AGZ00388.1 GI:45232563
GSS.
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AV832547.1 GI:14524636
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Best Local Similarity 77.8
Matches 14; Conservative
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AV832547/c
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organism="Mus musculus"
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/clone="IMAGE:1921297"
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/lab_host="DH10B"
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/strain="C57BL"
                                                                                                                                                       4 GCACAGCTGGGGAACAAGA 22
                                                                                                                                                                                                  26 GAACAGCTGGCGCAGAAGA 8
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EST.
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                                                           Local Similarity 78.9
nes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone was isolated from genomic DNA flanking an insertion of the P element vector P{GaWB} of a Drosophila strain.
nsertion position refers to the first base of the 8 base target
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/clone="NP3335-5-1"
/note="flanking P{GaWB} transposon insertion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.5%; Score 12.6; DB 10; Length 43; 78.9%; Pred. No. 6.6e+05; ive 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/mol_type="denomic DNA"
farzin="NP3335"
/db_xref="taxon:7227"
                                                                                                                                                           organism="Drosophila melanogaster"
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                                    recognition sequence.
Class: transposon insertion site.
                                                                                               Location/Qualifiers
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AG217348.1 GI:22764348
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AG217348/c
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/tau_nost__billo
/clone lib="Sigano mouse kidney mkia"
/clone lib="Sigano mouse kidney mkia"
/note="Organ: kidney: Vector: pMB18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
(ATGTGGCCTTTTTTTTTTTTTTTT); double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pMB18S-FL3
vector (5' site CACTGTGG, 3' site CACCATGG). Xhol should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sigano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACTGCAGCACA."
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S Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Riter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The Washlu-NCI Mouse EST Project 1999
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                       EST 18-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                A1527771 49 bp mRNA linear EST 18-MAR-1: uj28h01.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1921297 5' similar to TR:Q61314 Q61314 APOLIPOPROTEIN B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                  Gaps
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Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12.6; DB 1; Length 49; Pred. No. 6.6e+05;
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Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
                                                                  Indels
DB 10;
52.5%; Score 12.6; DB 10
78.9%; Pred. No. 6.6e+05;
iive 0; Mismatches 4
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Pred. No. 7.7e+05;
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           72.7%;
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              Best Local Similarity 72.74
Matches 16; Conservative
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Trace consi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi, Muroidea; Murinae; Mus.

E 1 (bases 1 to 25)
S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Reilly,M., Rose,M., St., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Stose,M., Stose,M.,
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1M0356N10F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0356N10 F, genomic survey sequence.
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                      Gaps
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                      Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0356 row: N column: 10
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0356N10"
/sex="Male"
                      Mismatches
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Location/Qualifiers
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Mus musculus
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                                                                                         2 ATGCACAGCTGGGGAACAA 20
                                                                                                                                      AZ511249.1 GI:10692565
                      15; Conservative
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                 RESULT 21
AZ511249/c
LOCUS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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51.7%; Score 12.4; DB 9; Length 25;

Query Match

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AA958372 20 08-MAY-1998 ualla03.12 Soares mammary gland Nahmom Mus musculus cDNA clone lualla03.13 46380 5' gimilar to TR:00111 00111 HYPOTHETICAL 28.2DA PROTEIN FROM HUMAN CHROMOSOME 19. [1] ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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1. (bases 1 to 28)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Tan,P., Wartin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseeer@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
Indels
0; Mismatches
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/mol_type="mRNA"
/strain="C57BL/63"
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/clone="IMAGE:1346380"
                                                2 ATGCACAGCTGGGGAACAAGAC 23
                                                                                              22 ACGAGCAGCCGGGAACACAAC 1
                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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5

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BH855497 16.20.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_085040.16.20.x, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab. host="B. Coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note=""Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/63 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                          E., SLC,
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.7%; Score 12.4; DB 9; 72.7%; Pred. No. 8.1e+05; iive 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 0082 row: C column: 24
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0082C24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: plasmid ends
High quality sequence stop: 42.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 72.7
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
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AUTHORS
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eguence of Brassica rapa ssp. pekinensis HindIII BAC clone
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                                                                                                                                                                                GSS 29-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                      Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="young leaves"
/lab_host="E.coli DH10B"
/clone lib="KBrH, Brassica rapa HindIII BAC library"
/note="vector: pcUGIBac1; Site 1: HindIII; Brassica rapa spp. pekinensis inbred line Chīifu BAC library (KBrH BAC) is provided by Yong-Pyo Lim."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZMO082C24R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0082C24 R, genomic survey sequence.
AZ814914.1 GI:12984822
GSS.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                           CW986355 SET 10 DNA linear GSS 29-DEC-200 KERH012L05R KBrH, Brassica rapa subsp. pekinensis genomic clone KBrH012L05, genomic survey
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Bark, J.Y., Lim, M.H., Kim, H.I., Lim, Y.P. and Park, B.S.
End sequence Of Brassica rapa HindIII BAC library (KBrH)
Unpublished (2004)
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/mol type="genomic DNA"
/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Beom-Seck Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Secdun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sub species="pekinensis"
|db_xref="taxon:51351"
|clone="KBrH012L05"
                                                                                                                                                                                                                                                                                                                                                    Brassica rapa subsp. pekinensis
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KBrH012L05
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                               CW986355
CW986355.1 GI:56852379
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                 14
                                          (bases 1 to 38)
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              GATGCACAGCTGGG
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Walbot, V.
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BH640991/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="SALK 085040.16.20.x"
/clone="SALK 085040.16.20.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana Inses
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 bp DNA linear GSS 30-JAN-200;
1007113H06.1EL_x1 1007 - RescueMu Grid H Zea mays genomic, genomic
Buf626386
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

( Dases 1 to 45)
Alonso,J.M., Leise,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeeke,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnollophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 100713 column: 24
                                                                                                                                                                                                                                                                                                                                            This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g09190. Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.7%; Score 12.4; DB 9; Length 45; 72.7%; Pred. No. 8.1e+05; ive 0; Mismatches 6; Indels
                                                                                                                                                      Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /moi_type="genomic_DNA"
/ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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BH626386
                                                                                                                                                                            JOURNAL
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                                                  REFERENCE
                                                                         AUTHORS
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                                                                                                                                       TITLE
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/dlone libe=1007 - RescueMu Grid H"
/clone libe=1007 - RescueMu Grid H"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site I: BamHI, Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.ramb.isatate.edu' and follow the links for
'RescueMu.' Grid H was grown at Berkeley in 2001. DNA
was extracted from leaf punches, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DHIOB cells were transformed and then screened on LB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH640991 49 bp DNA linear GSS 14-FEB-2002
1008039E08.1EL_x1 1008 - RescueMu Grid I Zea mays genomic, genomic
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1955 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walborGestanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008039 row: 29
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/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modifIed maize Mu transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 48;
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/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
                   /mol_type="genomic_DNA"
/cultivar="mixed background W23/A188/B73"
/tissue_type="leaf"
/dev_stage="leaf"
/lissue_type="leaf"
/dev_stage="adilt"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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72.7%; Pred. No. 8.2e+05;
tive 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Walbot V
Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .49
/organism="Zea mays"
'organism="Zea mays"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
/lab_host="DH108"
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Drosophila melanogaster (fruit fly)

Brosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Bracaoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bobydroidea; Drosophilae; Drosophila.

El (bases 1 to 49)

El (bases 1 to 49)

El (bases 1 to 49)

Enhibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,

Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,

Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.M.,

Greer, K., Hartouth, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K.,

Laufer, A., Mazcotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,

Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F.,

Swimmer, C., Kopczynski, C., Duyk, G., Winberg, M.L. and Margolis, J.

A complementary transposon tool kit for Drosophila melanogaster

using P and piggyBac

L. Nat. Genet. 36 (3), 283-287 (2004)
designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.radb.isstate.edu and follow the links for 'RescueMu,' Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and Bgllt, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS 29-APR-2005
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/strain="leogenic w- strain"
/db xref="teaxon:722"
/clone lib="Exelixis piggyBac PB insertions"
/clone lib="Exelixis piggyBac PB insertions"
/note="Vector: piggyBac PB (GenBank accession number
/note="Vector: piggyBac PB (GenBank accession number
AY515146); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the PB element using
Hsp70:piggyBac transposase from a single ammunition
element on either the X or third chromosome. We induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CO4702-3prime Exelixis piggyBac PB insertions Drosophila melanogaster genomic Sequence recovered from 3' end of piggyBac, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        piggyBac element.

The piggyBac insertion position is 1 in the 49 bases. This insertion position refers to the first base of the 4 base TTAA target recognition sequence.

Class: transposon insertion site.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Maillatop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 484 4015
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                           Score 12.4; DB 9; Length 49; Pred. No. 8.2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 TGCACACTTGAGCACCAGAAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TGCACAGCTGGGGAACAAGACG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CZ469449.1 GI:62963462
                                                                                                                                                                                                                                                                                                                                                        51.7%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                          16; Conservative
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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transposase expression by immersing bottles in a circulating 370C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."
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                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 17-JAN-2002
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/db_xref="taxon:5911"
/clone lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 18)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetrahymena thermophila
Eukaryota, Alveolata, Ciliophora, Oligohymenophorea,
Hymenostomatida, Tetrahymenina, Tetrahymenidae, Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM395302
50072-2-8-E01.r.1 Chilcoat/Turkewitz cDNA (large fraction)
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                                                                                                                                                                                                                                                                                      Length 49;
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                                                                                                                                                                                                                                                                                                                                 1; Indels

    .18
    /organism="Tetrahymena thermophila"
    /mol_type="mRNA"
    /strain="CU428.1"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetrahymena thermophila cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                    Score 12.4; DB 10;
Pred. No. 8.2e+05;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Chicago
920 E. 58th Street, Chicago, IL 60637,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: apturkew@midway.uchicago.edu
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 ACAGCTGGGGGCCCAGA 1
                                                                                                                                                                                                                                                                                      51.7%;
                                                                                                                                                                                                                                                                                                                                                                                 3 TGCACAGCTGGGGA 16
                                                                                                                                                                                                                                                                                                                                                                                                                          11 recacacereces 24
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 92.9
Matches 13; Conservative
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Fax: 773 702 3172
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nes 14; Conserv
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BM395302/c
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AA776443/c
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Matches
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Hominidae; Homo
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ORGANISM
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AA287473
           JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
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                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi;
Euarchontoglires; Primates; Catarrhini;
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ANG5D11, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1.

Location/Qualifiers
                                                                                                                                          1 (bases 1 to 36)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
Washl-NCI human EST Project
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                                                                                                                                                                                                                                                                        Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .36
/organism="Homo sapiens"
/ol_type="mRNA"
/db_xref="GDB:1390119"
/db_xref="taxon:9606"
/clone="IMAGE:453763"
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                   GI:2835777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
                                                       Homo sapiens (human)
                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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Best Local Similarity 82.47
Matches 14, Conservative
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Aspergillus niger
                                                                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                             Hominidae; Homo.
                                                                            Homo sapiens
AA776443
AA776443.1
               VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
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AJ239879
                                                                                                                                              REFERENCE
AUTHORS
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JOURNAL
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/use in the control of the control o
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 111 Std Error: 0.00
Seq primer: -28m13 rev2 Er from Amersham
High quality sequence stop: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /moi_type="mRNA"
/strain="ATCC6275"
/db_xref="taxon:5061"
/clone="AN05D11"
/clone_lib="Aspergillus niger ATCC6275"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.8%; Score 12.2; DB 1; 77.8%; Pred. No. 9.9e+05; tive 0; Mismatches 4;
transcribed genes in Aspergillus niger
Biotechnol. Lett. 21, 381-384 (1999)
Contact: Chae KS
                                                                                                                                                                                                                                                                                                                                                   1. .37
/organism="Aspergillus niger"
                                                                                                                                         Faculty of Biological Sciences
Chonbuk National University
Chonju 561-756, Republic of Korea.
Location/Qualifiers
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45 bp mRNA linear EST 08-DEC-2004 01792767 Antirrhinum majus cDNA clone 018 2 12 108, mRNA sequence. AJ792767 1 GI:51108095 EST.
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(bases 1 to 45)

Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
Saedler,H. and Zachgo,S.
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
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                                                                                                                                                                                                                                                                           /tissue_type="brain"
/clone_lib="3'-directed_mouse_cDNA_library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="018 2 12 108"
/tissue type="whole plant"
/clone_lib="Antixrhinum majus whole plant"
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Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5589
Fax: 81-743-72-5589
Email: kkato@bs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp,
Location/Qualifiers
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MPI fuer Zuechtungsforaschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:4151"
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                                                                                                                                                                                 1. .44
/organism="Mus musculus"
                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0006185"
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Antirrhinum majus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 CAATTGGGGAACAGGAC 22
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Best Local Similarity 82.4
Matches 14; Conservative
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Best Local Similarity
Matches 14; Conserv
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AJ792767
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AUTHORS
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I (basea) 1 to 43.
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Blurchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 44)
Kato, K. and Matoba, R. Generation of expressed sequence tags from mouse brain Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
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      went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
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42 bp mRNA linear EST
AV9577763 Nori Satoh unpublished cDNA library, egg Ciona
intestinalis cDNA clone cieg05k15 5', mRNA sequence.
AV957763
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                                                                              ch 50.8%; Score 12.2; DB 1; Length 41; I Similarity 82.4%; Pred. No. 1e+06; 14; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 42
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db xref="taxon:7719"
/clone="cieg05k15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
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Mus musculus
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                                                                                                                                                                7 CAGCTGGGGAACAAGAC 23
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Ciona intestinalis
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Best Local Similarity
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AU255694/c
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Benail: ysuzuki@ins.u-cokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
1-length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AU105507 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC12884, mRNA sequence.
                                                                                                                                                                                     Department of Virology
Institute of Medical Science, University of Tokyo
1-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@imsu-u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Suzuki, Y., Tairate, Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. Diverse transcriptional initiation revealed by fine, large-scale EMBO Rep. 2 (5), 388-393 (2001)
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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/db_xref="taxon:9606"
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82.4%; Pred. No. 1e+06;
iive 0; Mismatches 3;
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                                                                                                                                                                            Contact: Yutaka Suzuki
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Matches 14; Conserv
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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ov31"
/note="Toragan: ovary; Vector: pAMP1; mRNA made from ovarian carcinoms, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Non-amplified library. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui,
Tissue Procurement: W. Marston Linehan, Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium, LLNL
DNA Sequencid by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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AUI05506 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC12806, mRNA sequence.
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                                                       A1254367

qv33a10.x1 NCI CGAP Ov31 Homo sapiens cDNA clone IMAGE:1983354 3'
similar to gb:L21696 cds1 PROTHYMOSIN ALPHA (HUMAN);contains
TAR1.t1 TAR1 repetitive element ;, mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                   Hominidae, Homo.
1 (bases 1 to 49)
NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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82.4%; Pred. No. 1e+06;
ive 0; Mismatches 3; Indels
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AI254367.1 GI:3861892
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Homo sapiens
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1 (bases 1 to 50)
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Unpublished (1997)
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AU105506/c
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SM Gnetum gramon

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Gnetophyta; Gnetopsida; Gnetales; Gnetum.

Spermatophyta; Gnetophyta; Gnetopsida; Gnetales; Gnetum.

S berner, E. D., Twigg, R. W., Runko, S. J., Katari, M. S., Dedhia, N. N.,

O'Shaughnessy, A. L., Balija, V., Martienssen, R. A., McCombie, R. W.,

Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Gnetum female cone (NYBG)

Unpublished (2003)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8844

Fax: 516 367 8844

Email: mccombie@cshl.org

Seq primer: -21Ml3UnivRev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="Gnetum female cone (NYBG)"
/note="Organ: mature, unfertilized reproductive strobili;
/notes="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express CDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #416/84"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%; Score 12; DB 8; Length 33; 75.0%; Pred. No. 1.2e+06;
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/organism="Gnetum gnemon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:3382"
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                                     DN955268.1 GI:63027406
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                                                                                                                                                                                                                              REFERENCE
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//done designed to allow plasmid rescue from total genomic DNA.
//done follows:
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Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
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/mol_type="genomic_DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db xref="taxon:4577"
/tissue_type="leaf"
/dev stage="adult"
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                                        3; Indels
      1e+06;
      Pred. No. 1e+0; Mismatches
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/organism="Zea mays"
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Location/Qualifiers
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                                           14; Conservative
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Matches 14; Conserv
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Zea mays
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TITLE
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COMMENT
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0; Mismatches



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The invention relates to a novel method for detecting predisposition to high altitude pulmonary edema (HAPE). The method comprises amplifying intron 7 of the human inducible nitric oxide synthase (NOS) gene (ADZ75764) by designing and synthesizing forward and reverse oligonucleotide primers (ADZ75765+ADZ75766), and predicting and
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Adw69302 Forward p
Ady74734 KHCV enve
Adx77777 Livin RNA
Add05966 Human dia
Abv76929 Blocking
Adf72069 Human XPC
Ads74065 Tumour su
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Aax77148 Nerve mut
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Abz06705 Human leu
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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ACN71567 AAQ53128 AAT48684 AAV148684 AAV2056 AAV31314 ABL43141 ABL43141 ABL43141 ABL43154 ABJ22961 ABJ22961 ABJ22961 ABJ3371 ABN13371 ABN13373 ABN13373 ABN13374 ABN13375 ABN13375 ABN13376 ABN13376 ABN13376 ABN13377 ABN13376 ABN13377 ABN13377 ABN13377 ABN13378 ACN76465 ACN76465 ACN76465	ALIGNMENTS	ВР.	synthase gene	pulmonary edema; E iratory disease; SN					S INDIA.		high altitu inducible ferences i	English.
133 133 133 133 133 133 133 133 133 133		24 E	ry) oxide	pulmc raton			1313	1313,	IND RE		n to human g dif	13pp;
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		; DNA;	ent ric	itude resp:			2003US-00713137	2003US-00713137	CI &	. A;	Detecting predisposition amplifying intron 7 of hi predicting and analyzing variants.	3;
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		5766		s; PCR; high espiratory-ge rimer; exon.	sa 051(-MAY-	-NOV-	-NON-		a CI	ctin ify ict	щ 6;
0 1 0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		RESULT 1 ADZ75766 ID ADZ75766 XX ADZ75766 AC ADZ75766	28-JU	ss; PCR respira primer;	Homo sapiens US2005106573	19-M	13-N	13-N	(COUN-)	rasna WPI;	Dete ampl pred	Claim
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to new rodent beta-actin and ribosomal protein $21 (rp$21) promoters that have a low level of sequence homology to previously known Ba-actin and rp$21 promoters. The invention is based on the discovery that beta-actin promoters have higher promoter activity than CMV's promoter activity, and the discovery that the hamster rp$21 promoter is at least as active as the hamster Beta-actin promoter when used for expressing certain genes. The nucleotide sequences are useful as probes for screening genomic libraries for isolation of genomic sequences that hybridize to one or more of the promoter sequences or their
statistically analyzing differences in the distribution of the allelic variants in the populations, where GG genotype at 19480 position are at low risk of HAPE, and AA genotype at 19480 position are at high risk of HAPE. The present sequence represents the forward oligonucleotide primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New beta-actin and ribosomal protein S21 (rpS21) promoters, useful as enhancers and repressors for expression of heterologous nucleic acids encoding therapeutic proteins such as approximatelya-glucosidase, antibodies, and insulin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Forward primer for PCR of chinese hamster beta-actin promoter.
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                                                                                                                                        Seguence 24 BP; 8 A; 5 C; 9 G; 2 T; 0 U; 0 Other;
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100.0%; Pred. No. 0.2
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                               ADW69302 standard; DNA; 26
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1es 24; Conservative
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65.0%; Score 15.6; DB 14; Length 26; 81.8%; Pred. No. 2e+03;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Korean hepatitis C virus antigenic proteins - comprising epitopes of core protein, non-structural proteins or envelope protein, used for
                                                                                                                                                                                               E2A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Livin RNA used to prepare siRNA for therapy-resistant tumour therapy.
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丐
                                                                                                                                                                                             Korean-type hepatitis C virus; KHCV; HCV; envelope protein; E2E; epitope; diagnosis; primer; polymerase chain reaction; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                   Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15; DB 2; Length 38;
Pred. No. 3.9e+03;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Kim IS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 27; 91pp; English.
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23
                      22
 2 ATGCACAGCTGGGGAACAAGAC
                       1 AGGCCCAGCTTGGGACCAAGAC
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78.3%;
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                                                                                                                                                                         KHCV envelope primer PEIEGT2
                                                                           AAQ74734/c
ID AAQ74734 standard; cDNA; 38
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                                                                                                                                     (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-358190/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   DY,
                                                                                                                                                                                                                                                                                                                                                                                                   Choi
                                                                                                                                                                                                                                                                                                                                                                            (LUCK-) LUCKY
                                                                                                                                                                                                                                                                                                                            29-APR-1994;
                                                                                                                                                                                                                                                                                                                                                      30-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-DEC-2004
                                                                                                                                                                                                                                                                            WO9425486-A1
                                                                                                                                                                                                                                                                                                   10-NOV-1994.
                                                                                                                                     25-MAR-2003
26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis.
                                                                                                                                                                                                                                                   Synthetic.
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Best Local S:
                                                                                                              AAQ74734;
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                                                                                                                                                                                                                                                                                                                                                                                                      Cho JM,
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                                                               RESULT 3
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Human diacylglycerol kinase-zeta intron 22/exon 23 junction sequence.

(first entry)

31-JUL-2001

AAD05966;

AAD05966 standard; DNA; 20 BP.

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The present sequence corresponds to nucleotides 611-629 of the coding sequence of the livin (inhibitor of apoptosis protein) gene. Use of a nucleic acid containing this sequence, or its fragment of derivative, to prepare siRNA which sensitises therapy-resistant tumour cells for proposis is claimed. The siRNA is preferably delivered into a therapy-resistent tumour cells for apoptosis, and linker, to a complementary DNA strand. This is also used to prepare siRNA which sensitises therapy-resistant tumour cells for apoptosis, and is inserted into an expression vector with a cytostatic compound, death receptor ligand, death receptor invention are preferably used in combination with radiation therapy or antibody or negative regulator of anti-appoicts proteins. The therapy are sized to prepare sized to complementary DNA strand. With a cytostatic compound, death receptor ligand, death receptor intention are preferably used in combination with radiation therapy or antibody or negative regulator of anti-appoicts proteins. The therapy are sized to send and administry demonatous polyposis, hereditary non-polyposis colorectal. Coson, familiary adenomatous polyposis, hereditary non-polyposis colorectal. Cosonpagani, labial, laryngeal, hypopharynx, salivary and carcinoma, renal carcinoma, medullary thyroid carcinoma, errinoma, sendinal arynoma, medulary thyroid carcinoma, cervical carcinoma, strong carcinoma, strong carcinoma, strong carcinoma, strong parenchyma carcinoma, cervical carcinoma, strong parenchyma carcinoma, cervical carcinoma, strongeal, hypopharynx, salivary and carcinoma, passated carcinoma, selected carcinoma, erroinoma, ustrongement and carcinoma, selected carcinoma, melanoma, brain tumours proferably glioblascoma, astrocycoma, meningioma, medulloblastoma and corribarant lumours, Hodgkin's lymphoma, burkitt's lymphoma, acute lymphatic leukaemia (CML), acute myeloid leukaemia (AML), chronic carcinoma, pund sarcinoma, bronsida melanoma, melanoma, brain and preferably glioplascoma, choroidea melanoma, melanoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of a nucleic acid, or its fragment or derivative, for preparing Livin -specific siRNAs as an apoptosis inhibitor for the treatment of therapy-
Livin; inhibitor of apoptosis protein; short interfering RNA; siRNA; RNAi; gene silencing; cytostatic; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                Crnkovic-Mertens I, Hoppe-Seyler F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carcinoma or melanoma (all claimed).
                                                                                                                                                                                                                                                                                                                 (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 1; 22pp; English.
                                                                                                                                                                                                                     15-APR-2003; 2003EP-00008081
                                                                                                                                                                                                                                                                    15-APR-2003; 2003EP-00008081
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-730758/72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resistant tumors.
                                                                             Homo sapiens
                                                                                                                         EP1469070-A1
                                                                                                                                                                         20-OCT-2004.
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    %XCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCX
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                                                     Gaps
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                      Score 14.4; DB 13; Length 19;
Pred. No. 6.9e+03;
0; Mismatches 1; Indels (
Sequence 19 BP; 2 A; 7 C; 5 G; 0 T; 5 U; 0 Other;
                                                     0
                          60.0%;
93.8%;
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                                                     Conservative
                                   Local Similarity
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Best Loca Matches

AAD05966/c RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         namely diacylglycerol kinase epsilon, diacylglycerol kinase zeta, diacylglycerol kinase zeta-2 and their corresponding cDNAs. Human diacylglycerol kinase DNA is useful for coding human diacylglycerol kinase by his useful for catalysing the conversion of diacylglycerol kinase, which is useful for catalysing the conversion of diacylglycerol to phosphatidic acid. In particular, the human diacylglycerol kinase and its DNA are useful for decreasing intracellular levels of diacylglycerol (DAG) and for increasing intracellular levels of diacylglycerol codid in cells. The present DNA sequence is the exon/intron junction sequence of human diacylglycerol kinase (DGK) zeta gene
                                                                                                    Human; catalyst; diacylglycerol; DAG; phosphatidic acid; DAG modulator; diacylglycerol kinase zeta; DGK; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNAs of the human diacylglycerol kinase, useful for modulating the levels of diacylglycerol kinase in cells to catalyze the conversion of diacylglycerol to phosphatidic acid, therefore increasing phosphatidic acid levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The patent discloses novel human diacylglycerol kinase (DGK) isoforms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 1 A; 7 C; 5 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Topham M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Col 17-18; 74pp; English.
                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABV76929 standard; DNA; 30 BP.
                                                                                                                                                                                                                                                                                                                                                                                                        96US-0016210P.
97US-00841483.
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/number= 23
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/number= 22
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11. .20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Conservative
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/*tag=
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prescott SM,
                                                                                                                                                       Homo sapiens
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ID ABV7
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AC ABV7
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Synthetic.

Hoefer M,

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New nucleic acid encoding a p53 variant that can transactivate p21- and 14-3-3 aigma-promoter but not e.g. the PIG3-promoter, for obtaining complementary sequences capable of inhibiting expression of p53 variant and treating tumor.
                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for determining whether an age can be used to reduce the proliferation and/or cause the death of cance cells or inhibit the growth of a cancer cell population. The method is useful in determining whether an agent can be used to reduce the proliferation and/or cause the death of cancer cells or inhibit the growth of a cancer cell population. The present sequence represents a P primer which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                         Determining whether an agent can be used to reduce the proliferation, cause the death or inhibit the growth of cancer call population by obtaining a sample of cancer cells and quantifying the level of expression of a marker in the cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour; suppressor; p53; splice variant; cytostatic; gene therapy;
diagnosis; RT-PCR; primer; 88.
                                                                                                                                                                             Demuth JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.0%; Score 14.4; DB 10; Length 75.0%; Pred. No. 7.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 42 BP; 4 A; 14 C; 6 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                             Warner KA, Graves TG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour suppressor p53 RT-PCR primer EllR.
                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID NO 36; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GATGCACAGCTGGGGAACAAGACG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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                                       27-MAR-2003; 2003WO-US009428
                                                                          28-MAR-2002; 2002US-0368288P.
28-MAR-2002; 2002US-0368409P.
                                                                                                                                        (MEDI-) MEDICAL COLLEGE OHIO
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nes 18, Conservative
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                                                                                                                                                                           Weaver DA,
                                                                                                                                                                                                                                      WPI; 2003-902899/82.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-2004
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                                                                                                                                                                           Willey JC,
Crawford EL;
09-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes a nucleic acid synthesis reaction of selected regions of target nucleic acids from a group of two different target nucleic acids from a group of two different target nucleic acids. The method comprises combining in a reaction mixture, two different target nucleic acids, polymerase, additionally combining a blocking agent capable of binding a nucleic acid template molecule so template, and exposing the reaction mixture to a template, and exposing the reaction mixture to a temperature at which nucleic acids are synthesized by the polymerase. The method is useful for nucleic acid synthesize reactions, and is especially useful for creating DNA libraries. ABV16229-30 represent blocking oligonucleotides, which are used in the method of the invention to block amplification of the chymotrypain B precursor. The oligonucleotides are used to demonstrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proliferation; cancer; cancer cell growth inhibition; human; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preferential nucleic acid synthesis reaction of selected regions of target nucleic acids, by using a blocking agent which preferentially binds templates which are not desirable when amplifying the nucleic
                                                               Nucleic acid synthesis; blocking agent; polymerase; DNA library; chymotryptin B precursor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                       Blocking oligonucleotide #5 for chymotrypsin B precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 30 BP; 9 A; 2 C; 15 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GATGCACAGCTGGGGAACAAGACG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATGCACGGAGGGGAGGAGAGGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 6; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klink M;
                                                                                                                                                                                                                                                             24-APR-2001; 2001EP-00109971
                                                                                                                                                                                                                                                                                                    24-APR-2001; 2001EP-00109971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the method of the invention
                                                                                                                                                                                                                                                                                                                                         (LION-) LION BIOSCIENCE AG
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Kranz H,
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-077619/08
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hes 18; Conserv
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  03-MAR-2003
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Query Match Best Loc Matches

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The present sequence is that of RT-PCR primer E11R for the p53 tumour suppressor gene. RT-PCR was used to detect possible alternative splicing of p53 in different primate cell lines. A novel isoform of p53 (deltap53) was identified that is generated by alternative exon splicing. RT-PCR showed that deltap53 lacks 198 nucleotides from exons 7, 8 and 9. The coding exon 7 (nucleotide 767) and an acceptor site-like splicing-cassette within the coding exon 7 (nucleotide 767) and an acceptor site-like splicing-cassette within the coding exon 9 (nucleotide 965). The resulting trame. Thus, the novel p53-isoform lacks 66 amino acid residues from the central portion and hinge region of the protein but includes the functionally important C-terminal domain. The 984 bp cranscript of deltap53 is found in human, African green monkey and Rhesus monkey. Unlike full-length p53, the p53 splice variant is capable of transactivating the endogenous p21- and 14-3-3sigma promoter but not the mdm2-, bax- or P1G3 promoter. The invention provides means for inhibiting the proper that we have a provided the p53 variant contains a probe for a riboxyme, for a parcent the contains the parcent and the provides means for inhibiting the and parcent the activity of the p53 variant contains a probe for a riboxyme, for a parcent the contains the parcent and parcent parce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer therapy. Diagnostic compositions comprising a probe for detection of the splice variant are also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Constructing strains for identifying gene products as effective targets
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Candida albicans GRACE strain PCR primer SEQ ID NO 4498.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 7 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
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                         Example 1; SEQ ID NO 17; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GCACAGCTGGGGAACAAGA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCTCAGTGGGGGAACAAGA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABZ30347 standard; DNA; 22 BP
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20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roemer T, Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-566694/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida albicans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200253728-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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controlled by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous promoter. (M1) is useful for constructing a strain of diploid fungal cells having both alleles of a gene are modified. The diploid fungal cells having both alleles of a gene are modified. The diploid fungal contributes to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a fungus and for identifying a therapeutic agent for treatment of a mammalian chaese. (M1) is useful for identifying a compound which modulates the compound catabolism, blosyntheric, transporter, transcriptional, compound catabolism, blosyntheric, transporter, transcriptional, craning infection by C. albicans. The present sequence is that of a PCR treating infection by C. albicans. The present sequence data for transprant of the survice of this patent is not represented in the printed apportant of a passed for treating infection by C. albicans. The present sequence data for this patent is not represented in the printed apportant of the present control of the control of the proposed patents and the control of the control of the proposed patents and the control of the control of the proposed patents and the control of the contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on sequence information supplied to Derwent by the European Patent Office
cells in which both alleles of a gene are modified, comprising modifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutation factor; chromosome 10; glioma; tumour suppressor; tumour; astrocytoma; gene therapy; human; mouse; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila neuralized gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.2; DB 6; Length 22;
Pred. No. 8.7e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human gene on chromosome 10 homologous to Drosophila neur useful in the diagnosis and gene therapy of brain tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22 BP; 6 A; 2 C; 9 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nerve mutation factor DNA amplifying primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saya
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page 25; 78pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SUME ) SUMITOMO ELECTRIC IND CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GATGCACAGCTGGGGAACA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGGAGAGCTGGTGAACA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВР.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 59.2%;
1 Similarity 84.2%;
16; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX77148 standard; DNA; 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-347474/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nerve mutation
brain tumour; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX77148;
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Best Local S
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(BIOC-) BIOCARDIA INC.
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                                                                                                                                                                                        WO200257414-A2.
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                                                                                                                                                                  Homo sapiens.
                                                                09-JAN-2003
                                                                                                                                                                                                            25-JUL-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Si
Matches 16,
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                                           ABZ06705;
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RESULT 12
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           ABZ06705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding a bio catalyst which desulphurises fossil fuels - obtd. from Rhodococcus rhodochrous bacteria, used to produce microorganisms which degrade organic sulphur cpds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA obtained from Rhodococcus rhodochrous encodes enzymes/biocatalysts which can desulphurise fossil fuels (See AAG51131, AAG55132).
Microorganisms transformed with the DNA can be used to produce the enzymes/biocatalysts for the selective oxidative cleavage of carbonsulphur bonds for desulphurisation of fossil fuels which contain organosulphur compounds. Two primers (AAG55125, AAG55125) were used to amplify the sequence designated as open reading frame 1 (ORF 1) of the DNA descibed in AAQ55131. (Updated on 25-MAR-2003 to correct PN field.)
(AAY21558 and AAY21559) are provided. The protein is believed to have tumour suppressor activity. Polymucleotide sequences and antibodies to the protein are diagnostic reagents for highly malignant brain tumors such as astrocytoma where chromosome 10 deletion commonly occurs. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                         Primer for sequence coding enzymes which desulphurise fossil fuel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.2%; Score 14.2; DB 2; Length 37; 84.2%; Pred. No. 9.4e+03; live 0; Mismatches 3; Indels
                                                                                      Score 14.2; DB 2; Length 23; Pred. No. 8.8e+03;
                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Young KD,
                                              gene may also be used for gene therapy of such tumours
                                                                                                                                                                                                                                                                                                                Enzyme; biocatalyst; fossil fuel; oxidation; cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37 BP; 8 A; 8 C; 12 G; 9 T; 0 U; 0 Other;
                                                                  Sequence 23 BP; 2 A; 6 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piddington CS, Kovacevich BR,
                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 5; Page 61; 104pp; English.
                                                                                                                                                                                                                                                                                                                           organosulphur compounds; coal; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GCACAGCTGGGGAACAAGA 22
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                                                                                                                                 5 CACAGCTGGGGAACAAGAC 23
                                                                                                                                                19 CCCAGCTGAGGAACAAGCC 1
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                                                                                                                                                                                                               BP.
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                                                                                        59.2%;
84.2%;
                                                                                                                                                                                                               AAQ55126 standard; DNA; 37
                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                Query Match
Best Local Similarity 84.29
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                      WO9401563-A1
                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                            20-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rambosek J,
                                                                                                                                                                                                                                                         25-MAR-2003
02-AUG-1994
                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                    AAQ55126;
                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                     AAQ55126
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                                                                                                                                                                                                                                                                                  17, leukocyte; gene expression profiling; allograft rejection;
atherosclerosis; congestive heart failure; systemic lupus erythematosus;
rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
Ly N, Woodward R, Quertermous T, Johnson F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                Human leukocyte gene expression profiling probe SEQ ID NO 6696.
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Pred. No. 9.8e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 545; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 ACAGCTGGGAACAAGACG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ACAGCTGAAGAACAAGAAG 20
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ABZ06705 standard; DNA; 50
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                                                                                                                                               (first entry)
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ABZ07095 standard; DNA;
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Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ65654 to AAZ69578 represent human biallelic markers from the present
                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of a Streptococcus pneumoniae surface protein, called SpsA, that binds to secretory IgA The sequences can be used in vaccines for treating pneumococcal infections. The present sequence is a PCR primer used to isolate the coding sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                Pneumococcal surface protein SpsA - for use in producing vaccines,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                       ch 58.3%; Score 14; DB 2; Length 37; 1 Similarity 77.3%; Pred. No. 1.2e+04; 17; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37 BP; 12 A; 10 C; 13 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human map-related biallelic marker SEQ ID NO:1997.
                                                          (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 656; 2745pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GATGCACAGCTGGGGAACAAGA 22
                                                                                                                                                                                                                          Example 6; Page 5-6; 12pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 garccacagecregaaacaaga 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ67650 standard; DNA; 47 BP
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                    97DE-01008537.
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                                                                                                  Hammerschmidt
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                                                                                                                                        WPI; 1998-481924/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                    03-MAR-1997;
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                                                                                                Chhatwal GS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-SEP-2001
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variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ67650;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus,
T7; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumococcal; surface protein; secretory IgA; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                  Phillips J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                    Altman P, Prentice J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 50 BP; 10 A; 15 C; 9 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                       Johnson F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pneumoniae SpaA gene PCR primer SH24.
                                                                                                                                                                                                                                                                                                                                                                  muth J, Fry K, Matcuk G, A
Woodward R, Quertermous T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 556; Opp; English.
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                                                                                                                                                                                                                                                                20-OCT-2000; 2000US-0241994P.
08-JUN-2001; 2001US-0296764P.
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                                                                                                                                                                                                                          22-OCT-2001; 2001WO-US047856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                             (BIOC-) BIOCARDIA INC
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                                                                                                                                          WO200257414-A2
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                                                                                                    Homo sapiens
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SpaA;

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Matches

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treatment in an individual. The diseases include cardiac allograft

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invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ7440 represent amplification primers for the biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and disgnostic methods, as well as the characterisation of the dharmaceutical efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment.

N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and and also, accusally given a sequence in the Sequence Listing from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; leukocyte; gene expression profiling; allograft rejection;
atherosclerosis; congestive heart failure; systemic lupus erythematosus;
rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human leukocyte gene expression profiling probe SEQ ID NO 6394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prentice J,
                                                                                                                                                                                                                                                                                                             Sequence 47 BP; 16 A; 13 C; 6 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Altman P,
T, Johnson F
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Quertermous T,
                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ATGCACAGCTGGGGAACAAGAC 23
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08-JUN-2001; 2001US-0296764P.
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Woodward R,
                                                                                                                                                                                                                                                                         present invention
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
              rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
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rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
                                                      rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human leukocyte gene expression profiling probe SEQ ID NO 6784.
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                                                                                                                                  58.3%; Score 14; DB 6; Length 50; 100.0%; Pred. No. 1.2e+04; tive 0; Mismatches 0; Indels
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                                                                                          Sequence 50 BP; 16 A; 8 C; 19 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wohlgemuth J, Fry K, Matcuk G, A Ly N, Woodward R, Quertermous T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 547; Opp; English.
                                                                                                                                                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                                                                                                                                                                               ABZ06793 standard; DNA; 50
                                                                                                                                                                                                                      9 GCTGGGGAACAAGA 22
                                                                                                                                                                                                                                                            31 GCTGGGGAACAAGA 44
                                                                                                                        Query Match
Best Local Similarity 100.u
....hes 14; Conservative
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RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                                                                                                                              Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                                                                                                                                           Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8469.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 8469; 214pp; English.
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                                                                                                                                                       ABN08477 standard; DNA; 17 BP.
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30-JAN-2001; 2001WO-US000663.
30-JAN-2001; 2001WO-US000664.
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30-JAN-2001; 2001WO-US000661.
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                    GCTGGGGAACAAGA 22
                                                                                                                                                                                                                                    (first entry)
                                          GCTGGGGAACAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-179446/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AEOM-) AEOMICA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200192524-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ji Y,
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2000;
                                                                                                                                                                                                                                    29-MAY-2002
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                                                                                                                    RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid sequences associated with tumor suppression, regression, apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.
The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with tumour suppression or regression, apoptosis or virus resistance. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents an isolated nucleic acid sequence associated
                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss; tumour suppressor; antitumour; cytostatic; tumour suppression; tumour regression; apoptosis; virus resistance; diagnosis; cellular degeneration.
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                                                                                                                                                                                                                                                                              2; Indels
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88.2%; Pred. No. 1.3e+04;
ive 0; Mismatches 2;
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                                                                                                                                                                     Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                     57.5%; Score 13.8; DB 6; 88.2%; Pred. No. 1.3e+04;
                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                               ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tumour suppressor sequence #1473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amson R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR ENGINES LAB
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                                                                                                                                                                                                                                                                                                                                       8 AGCTGGGGAACAAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACC52706 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 57.5
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-250498/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JUN-2003
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Gaps

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Indels

ACN71567;

ACN71567

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The sequences (AAQ53077-Q53136) are used in the invention to detect specific genes without the use of radio-isotopes. Detection is carried out by hybridisation of denatured (ss) sample DNA with a (ss) nucleic acid probe, complementary to the target sequence. Hybridisation occurs on the surface of an electrode or optical fibre and detection is visualised by the addition of an entity that recognises (ds) hybridised DNA and is
                                                                                                                                                                                                                                                                                                                  Gene detection; radio-isotopes; target gene; electrode; detection; optical fibre; hybridise; hybridisation; electrochemical; photochemical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection method of gene without using radio-isotope - by hybridisation of nucleic acid probe which is single strand having complementary sequence of gene and single strand denatured sample DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe for detecting N-ras gene mutations in the codon at position 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutated codon, single base mutation, human, acute myeloid leukaemia, tumour, activated ras gene, N-ras, H-ras, K-ras, 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 9 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.8; DB 2;
Pred. No. 1.3e+04;
0; Mismatches 2;
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7
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Mismatches
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                                      24
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                                                                                                                                                                    BP
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88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duery Match
Bust Local Similarity 88.40,
                                                                        1 AGCTGGAGAACATGACG
                                                                                                                                                                    AAQ53128 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 ACAGCTGGGGAACAAGA
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                                      8 AGCTGGGGAACAAGACG
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                                                                                                                                                                                                                                                                               Gene detection sequence 52
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                                                                                                                                                                                                                                           (first entry)
   15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT48684 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                        electrolysis; probe; ss
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                                                                                                                                                                                                                                           03-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-1992;
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02-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                        AAQ53128;
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ID AAT48
XX
AC AAT48
XX
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DT 25-MA
DT 25-MA
DT 02-OC
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MULAL
KW LUMOU
   Matches
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                                                                        임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel polypeptide (I) comprising a sequence (SI) of wyosin-like protesin-1 (hgbubr-1) having 2568 amino acids fully defined in the specification, a fragment of at least 8 amino acids fully (SI), 95% deviation from (SI) which are conservative substitutions, and esk identity to (SI). A polypeptide of the invention acts as a agonist or antagonist of hgbur-1, or as an inhibitor of hGbur-1 activity. A pharmaceutical composition of the invention is useful for treating or hGbwip-1, such as a disorder of heart and/or skeletal muscle function. The present sequence represents a 17-mer nucleotide, used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                                                                                                                                       Human; 88; probe; myosin-like protein-l; hGDMLP-l;
hGDMLP-l agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
skeletal muscle function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shannon ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.5%; Score 13.8; DB 13; Length 17; 88.2%; Pred. No. 1.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention for scanning the sequence represented in ACN63103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, SEQ ID NO 8469; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                  Human GDMLP-1 probe SEQ ID NO:8469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001MO-US000665.
2001MO-US000666.
2001MO-US000667.
2001MO-US000669.
2001MO-US000669.
2001MO-US000670.
                      ACN71567 standard; DNA; 17 BP
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2000US-0236359P.
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2001WO-US000662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000GB-00024263
                                                                                           (first entry)
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HANZEL D K.
RANK D.
CHEN W.
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Best Local Similarity
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30-JAN-2001;
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30-JAN-2001;
30-JAN-2001;
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                                                                                                                                                                                                                                               Homo sapiens
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                                                                                             02-DEC-2004
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Gaps

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Function

(RANK/) (CHEN/)

(HANZ/)

(SHAN/)

Gu Y,

(COXX/) (JIYY/)

Length 20; Indels

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containing a mutated codon. The method involves: either cleaving a human subject sequence from the method involves: either cleaving a human containing a mutated codon. The method involves: either cleaving a human subject sequence cooperation enzyme to produce DNA fragments and treating the fragments to obtain single-stranded DNA molecules or poly4+ mRNA under hybridising conditions with a labelled synthetic DNA molecule, optionally bound to a solid support, comprising 12-20 nucleotides, where the synthetic DNA molecule is 5'-B-Q-D-3' in the case of single-stranded DNA or is complementary to 5'-B-Q-D-3' in the case of poly4+ mRNA B = 0.9 nucleotides having a sequence complementary to case of poly4+ mRNA B = 0.9 nucleotides having a sequence complementary to a sequence in the activated ras gene 5' of the mutated codon, D = 0-12 nucleotides having a sequence complementary to a sequence in the cativated ras gene 5' of the mutated codon, provided that B and D contain a total of at least 9 nucleotides, and Q is complementary to the mutated codon, treating the presence of the labelled synthetic DNA molecule in the certing the presence of the labelled synthetic DNA molecules. The present sequence represents the synthetic DNA probe used for detecting the activated N-ras gene when the mutated codon can be used for the diagnosis of acute myeloid leukaemia conditions can dother tumours. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                              Detection of activated ras gene - using oligo:nucleotide probes to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.5%; Score 13.8; DB 2; Length 20; 88.2%; Pred. No. 1.3e+04; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe; N-ras; mutation detection; mismatch binding protein; cancer diagnosis; single strand binding protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; Col 29; 20pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 ACAGCTGGGGAACAAGA 22
                                                                                                                        94US-00264425.
                                                                                                                                                            85US-00758104
                                                                                                                                                                             87US-00081490
92US-00873352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-1998 (first entry)
                                                                                                                                                                                                                                    (UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Conservative
                                                                                                                                                                                                                                                                          Van Der Eb AJ, Bos JL;
                                                                                                                                                                                                                                                                                                          WPI; 1997-086629/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                   mutated codon.
                                                                                                                          23-JUN-1994;
                                                                                                                                                              23-JUL-1985;
                                                                                                                                                                               04-AUG-1987;
21-APR-1992;
                                                   US5591582-A.
                                                                                      07-JAN-1997
                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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This sequence represents a probe for the N-ras gene, that can be used in the method of the invention. The method is for for detecting a mutation from a non-mutated sequence of a target polymucleotide (TP) in a sample, by using a mismatch binding protein (MBP), comprises: (a) providing a non-mutated and mutated TP; (b) forming duplex of the non-mutated and compared of TP in (a); (c) adding a single strand binding continuated single strands of TP in (a); (c) adding a single strand binding contivating agent; (e) adding the incubated MBP from (d) to the polymucleotide from (c), so that MBP binds to the duplex formed by one con-mutated and one mutated single strand of TP; and (f) detecting the presence of any MBP bound to TP. The method may be used for early changes is of cancer. Binding of MBP to single strands is inhibited by the single strand binding protein. By activating MBP with an activator, before addition to the sample, binding to double strands lacking
                                                                                                                                                                                                                                 Method for detecting mutation(s) by mismatch binding protein - useful for separating mutation from non-mutated target polynucleotide in sample,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.5%; Score 13.8; DB 2; Length 20; 88.2%; Pred. No. 1.3e+04; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ras oncogene; probe; point mutation; detection; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                 used in early diagnosis of cancer.
                                                                                                                                                                                                                                                                                                Disclosure; Page 9; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mismatches does not take place
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87US-00081490.
92US-00873352.
94US-00264425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 ACAGCTGGAGAAGA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ras oncogene probe #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00778543
                                                                          97WO-SE000839.
                                                                                                       96SE-00002062
                                                                                                                                      (PHAA ) PHARMACIA BIOTECH AB
                                                                                                                                                                     Tosu M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 ACAGCTGGGGAACAAGA
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                    WPI; 1998-130209/12.
                                                                                                                                                                     Goto M,
                                                                          22-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-AUG-1987;
21-APR-1992;
23-JUN-1994;
                                                                                                         29-MAY-1996;
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              WO9745555-A1
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                                          04-DEC-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                      Hasebe M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV73038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 24
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The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in method comprises: (a) clones of the genomic libraries contained in contained in amiliaries numbered for discrimination are mixed in each of the multiwell plates; (b) a primer designed based on the chromosome marker contained; (c) a asjonal corresponding to the marker is detected from the resultant containing the clones having said marker sequence; (d) the order of the marker is changed so that the same discrimination Nos. or example of the multiwell containing the clones in the multiwell plates of the specified discrimination Nos. to array the multiwell containination Nos. to array the multiwell cand lateral directions; (f) the mixed clones are cultured and the canditation to the amplified by using the above primer; (g) signals can edetected from the amplified by using the above primer; (g) signals can edetected from the amplified products; (h) the clones in the multiwell plates are specified from the amplified products; (h) the clones are cultured and the constituted as the positions on the chromosome and arrayed. The constituted as the positions on the chromosome and arrayed. The constituted is useful for gene analysis. ABL42597 to ABL45321 represent propresent promessed to the present invention can be present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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               Length 20;
                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Human chromosome 1p36-35 PCR primer SEQ ID NO:598.
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               Score 13.8; DB 2;
Pred. No. 1.3e+04;
57.5%; Scor.
88.2%; Pred. No. 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTGGTGAAGAAGACG 20
                                                                                                        22
                                                                                                                                                                                                                                                             BP.
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                                                                                                                                    20 ACAGCTGGAGAAGAGA
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                                                                                                                                                                                                                                                             ABL43554 standard; DNA; 20
                                                                                                        ACAGCTGGGGAACAAGA
                                                                                                                                                                                                                                                                                                                                                 11-APR-2002 (first entry)
                  Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arraying genome clones.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENO-) GENOTEX YG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                      AAV73026-V73071 are probes used to detect a single-base mutation in a human ras oncogene. These probes comprise 12-43 nucleotides of formula 5' -26-D-3', Q = 3 nucleotides complementary to the mutated codon, and B and D each = 0-20 nucleotides complementary to the ras sequences flanking the mutated codon. The probes are useful for detecting cancers associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                               Probes for detecting ras oncogene point mutations - useful for the diagnosis of cancer associated with single base mutations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ras oncogene mutant detecting oligomer N-61a.
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 9 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 ACAGCTGGGGAACAAGA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAGCTGGAGAGAAGA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV73141 standard; DNA; 20 BP
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87US-00081490.
92US-00873352.
94US-00264425.
                                                                                                                                                                                                 Claim 6; Col 5; 18pp; English
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Matches 15, Conservative
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  (UYLE-) RIJKSUNIV LEIDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Der Eb AJ;
                                           Van Der Eb AJ;
                                                                                                                                                                                                                                                                                                                                                      with point mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-059149/05.
                                                                                    WPI; 1999-059149/05
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04-AUG-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                           Bos JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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Synthetic

ADJ22962;

RESULT 27

ADJ22962

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New antisense oligonucleotide for modulating endothelial lipase expression, for diagnosing, preventing or treating e.g. dyslipidemia, low high density lipoprotein or cardiovascular disorders.
                                                                                                                       Antilipaemic, Cardiovascular, Analgesic, Antianginal, Antisense therapy;
Human, Endothelial Lipase, dyslipidaemia, high density lipoprotein; HDL;
cardiovascular disorder; metabolic syndrome X; ss.
                                                                                                                                                                                                                                                                                                                                        /mod_base= OTHER
/note= "This oligonucleotide has a phosphorothioate
backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5'
and 3' ends, which are 4 nucleotides in length. Also all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human endothelial lipase antisense oligonucleotide, SEQ ID 1359.
                                                                                Human endothelial lipase antisense oligonucleotide, SEQ ID 1696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.5%; Score 13.8; DB 12; Length 20; 88.2%; Pred. No. 1.3e+04; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ22961 standard; DNA; 20
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                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-132912/13.
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                                                                                                                                                                                                                                                                             Key
modified_base
                                                                                                                                                                                                              sapiens
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                                        20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2004
                                                                                                                                                                                                                                   Synthetic.
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ADJ23298;
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                                                                                                                                                                                                              Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense oligonucleotide for modulating endothelial lipase expression, for diagnosing, preventing or treating e.g. dyslipidemia, low high density lipoprotein or cardiovascular disorders.
                                                                                                                                                                                                                                                     Antilipaemic, Cardiovascular; Analgesic; Antianginal; Antisense therapy;
Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
cardiovascular disorder; metabolic syndrome X; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "This oligonucleotide has a phosphorothioate backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5' and 3' ends, which are 4 nucleotides in length. Also all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are
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                                                                                                                                                                                                              Human endothelial lipase antisense oligonucleotide, SEQ ID 1360.
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Pred. No. 1.3e+04;
0; Mismatches 2; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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/mod_base= OTHER
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                                                                                   ADJ22962 standard; DNA; 20 BP.
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Matches 15; Conserv
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modified_base
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Bhat BG;

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Gaps

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Query Match

RESULT 28

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ADJ23298 ID ADJ2 XX

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Location/Qualifiers
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                                                                                                               WO2004009541-A2
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            Key
modified_base
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                                                                                                                                    29-JAN-2004
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                                                                                                                                                                                                                            Bhat BG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                            /mod_base= OTHER
/note= "This oligonucleotide has a phosphorothioate
backbone and 2-'methyoxyethyl (2'-NOE) wings at the 5'
and 3' ends, which are 4 nucleotides in length. Also all
cytidine residues are 5-methylcytidines"
Antilipaemic, Cardiovascular; Analgesic; Antianginal; Antisense therapy; Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL; cardiovascular disorder; metabolic syndrome X; ss.
                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for disgnostics, prophylaxis, or as research reagents or kits.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.5%; Score 13.8; DB 12; Length 20; 88.2%; Pred. No. 1.3e+04; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 4 A; 3 C; 11 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; SEQ ID NO 1359; 1007pp; English.
                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                    19-JUL-2002; 2002US-0397106P
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Res 15; Conserv
                                                                                                                                                                                  WO2004009541-A2
                                                                               Key
modified_base
                                            Homo sapiens.
Synthetic.
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Matches
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/mod_base= OTHER
/mode= "This oligonucleotide has a phosphorothioate
/mode= "This oligonucleotide (2'-MOE) wings at the 5'
backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5'
and 3' ands, which are 4 nucleotides in length. Also all
cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to antisense oligonucleotides (ADJ21603-ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence (ADJ25517), where the antisense oligonucleotide specifically hybridises with and inhibits the expression of EL. The antisense oligonucleotides are useful for modulating the expression of endothelial lipase in cells or tissues to treat diseases associated with EL expression, such as dyslipidaemia, low high density lipoprotein (HDL), cardiovascular disorder or metabolic syndrome X. In addition, the oligonucleotides are used for diagnostics, prophylaxis, or as research reagents or kits.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 1.3e+04;
0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 5 A; 3 C; 11 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; SEQ ID NO 1929; 1007pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                        18-JUL-2003; 2003WO-US022410.
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nes 15, Conservative
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gene therapy; vaccine; heart disease;

muscle; myosin; chromosome 22; gene therapy; vacci skeletal muscle disorder; amplicon; screening; ss.

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids in samples, as amplification substrates, to nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be capture as immunosens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP-proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The concurrance associated with the expression of hGDMLP-1, in particular heart can skeletal muscle disorders. hGDMLP-1 may be used for diagnosing a configuration of the present sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. at fip.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                                                                                                                                                                        Shannon ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.5%; Score 13.8; DB 6; Length 25; 88.2%; Pred. No. 1.4e+04; ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25 BP; 8 A; 6 C; 9 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                        Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 13363; 214pp; English.
                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                     2001WO-US000665.
2001WO-US000666.
                                                                                                                                                                                                                                    2001WO-US000669.
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                                                                                           2001WO-US000662
2001WO-US000663
                                                                                                                                    2001WO-US000664
                                                                                                                                                                                            2001WO-US000667
                                                                                                                                                                                                               2001WO-US000668
                               2000US-0236359P
                                                     2000GB-00024263
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nes 15, Conservative
                                                                                                                                                                                                                                                                                                                                                        Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-179446/23.
                                                                                                                                                                                                                                                                                                                  (AEOM-) AEOMICA INC.
                                                                                           30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
                                                                                                                                                   30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                          Ji Y,
                                                                                                                                                                                                                                    30-JAN-2001;
                                                                        30-JAN-2001;
                                                     04-OCT-2000;
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Matches
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New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.

Disclosure; SEQ ID NO 13364; 214pp; English.

Chen W, Shannon ME;

Rank DR,

Hanzel DK,

Gu Y, Ji Y, Penn SG, WPI; 2002-179446/23.

(AEOM-) AEOMICA INC.

30-JAN-2001; 2001WO-US000664. 30-JAN-2001; 2001WO-US000665. 30-JAN-2001; 2001WO-US000666. 30-JAN-2001; 2001WO-US000667. 30-JAN-2001; 2001WO-US000669. 30-JAN-2001; 2001WO-US000669.

2001US-0266860P

05-FEB-2001;

2000US-0207456P. 2000US-0234687P. 2000US-0236359P.

25-MAY-2001; 2001WO-US016981

WO200192524-A2

06-DEC-2001

Homo sapiens.

2000GB-00024263

27-SEP-2000; 04-OCT-2000;

30-JAN-2001; 2001WO-US000661 30-JAN-2001; 2001WO-US000662 30-JAN-2001; 2001WO-US000663

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the present invention to the control genome-cative myosthritate protein 1 (AGDMLP-1). The protein and polymucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, controlled initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP-1 proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The capture sequence sencoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart can delebetal muscle disorders, hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the CTDMLP-1 sequence of the printed continuation of the present invention. N.B. The sequence data for this patent did not form part of the printed continuation of the present invention. The protein of the present sequence and present sequence data for this patent did not form part of the printed continuation that the continuation of the present sequence and present sequence data for this patent did not form may part of the printed continuation that the continuation of the present sequence data for this patent and part of the printed continuation that the continuation that the continuation that the co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a human genome-derived myosin-like
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Pred. No. 1.4e+04;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25 BP; 7 A; 6 C; 10 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequence
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Best Local Similarity 88.2
Matches 15; Conservative
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Gaps

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24

8 AGCTGGGGAACAAGACG AGCTGGAGAACATGACG

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23

AGCTGGAGAACATGACG 22

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Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;

Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13364.

(first entry)

29-MAY-2002

2×2×2×2×4

ABN13372;

BP.

ABN13372 standard; DNA; 25

RESULT 32 ABN13372

29-MAY-2002

ABN13376;

ABN13376

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Sequence 25 BP; 9 A; 5 C; 9 G; 2 T; 0 U; 0 Other;
                                                                                                                                             15; Conservative
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                                                             Query Match
Best Local Similarity
Matches 15; Conserv
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The present sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO can fire.
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                                                                                                                                                                                                                                                                                                                                                        Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                                                                                                                                                          Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13368.
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2001WO-US000663.
2001WO-US000664.
2001WO-US000665.
2001WO-US000665.
                                                                                   ABN13376 standard; DNA; 25 BP.
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2001WO-US000669
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2000US-0236359P
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30-JAN-2001;
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30-JAN-2001; 30-JAN-2001; 30-JAN-2001; 30-JAN-2001;

04-OCT-2000; 27-SEP-2000

26-MAY-2000;

06-DEC-2001

Homo

30-JAN-2001; 30-JAN-2001; 30-JAN-2001; 30-JAN-2001;

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically, recognise hGDMLP-1 proteins as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as
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                                                                                                                                                                                                                                                                                                                    Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; 88.
                                     Gaps
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Score 13.8; DB 6; Length 25;
Pred. No. 1.4e+04;
0; Mismatches 2; Indels
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1.4e+04;
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                                                                                          |||||||| |||||| |||||| AGCTGGAGAACATGACG 18
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30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000668.
   57.5%;
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therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polymucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
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Pred. No. 1.4e+04;
0; Mismatches 2; Indels
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                                                                                                                                                                             Sequence 25 BP; 8 A; 5 C; 10 G; 2 T; 0 U; 0 Other;
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30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001WO-US000669.
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88.2%;
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Best Local Similarity 88.2
Matches 15; Conservative
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27-SEP-2000;
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nucleic acids can be used as probes to detect, characterise and quantify nucleic acids can be used as probes to detect, characterise and quantify convice initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polyapeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specifically of hGDMLP-1 capture probes for surface-enhanced laser desorption ionisation, as the reaching specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The present sequence encoding hGDMLP-1 may be used for diagnosing a clisorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence in the exemplification of the present invention. N.B. The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from MIPO
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protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 AGCTGGAGAACATGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABN13377 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 57.5
Best Local Similarity 88.2
Matches 15; Conservative
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30-JAN-2001;
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27-SEP-2000;
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WO200192524-A2
                     30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
                                                                                                                                                                                                                                                         Ji Y,
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  30-JAN-2001;
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                                                                                                                                                                                                                                                         Gu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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The present sequence represents an oligomer used in the screening of the hospit. sequence data for this patent did not form part of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at fig.
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                                                                                         New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
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  Shannon ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.5%; Score 13.8; DB 6; Length 25; 88.2%; Pred. No. 1.4e+04; ive 0; Mismatches 2; Indels
  Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 10 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
  Rank DR,
                                                                                                                                                                                        Disclosure; SEQ ID NO 13369; 214pp; English
  Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AGCTGGGGAACAAGACG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABN13369 standard; DNA; 25 BP.
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2001WO-US000662.
2001WO-US000663.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.2
Gu Y, Ji Y, Penn SG,
                                                WPI; 2002-179446/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200192524-A2.
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30-JAN-2001;
30-JAN-2001;
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27-SEP-2000;
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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids in samples, as amplification substrates, to nucleic acids can be used as probes to detect, characterise and quantify CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be capture probes immunospens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP-proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionication, as therapulation and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The concentration and skeletal muscle disorders. hGDMLP-1 may be used for diagnosing a clisorders associated with the expression of hGDMLP-1 in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the CDMLP-1 sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO cat fitp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Shannon ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 13361; 214pp; English.
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                                                                                                                                                  2001WO-US000668.
2001WO-US000669.
2001WO-US000670.
                                    2001WO-US000665.
2001WO-US000666.
2001WO-US000667.
                                                                                                                                                  30-JAN-2001; 2001WO-US000668
30-JAN-2001; 2001WO-US000669
30-JAN-2001; 2001WO-US000669
35-FEB-2001; 2001US-0266860P
2001WO-US000664
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es 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG,
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Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.

Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13367.

25-MAY-2001; 2001WO-US016981.

06-DEC-2001

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57.5%; Score 13.8; DB 6; Length 25; 88.2%; Pred. No. 1.4e+04; ive 0; Mismatches 2; Indels
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                                                        2001WO-US000662.
                                                                                 2001WO-US000666.
2001WO-US000667.
                                                                                               2001WO-US000668.
                                                                                                      2001WO-US000669.
                                                                                                           2001WO-US000670.
2001US-0266860P.
                         2000US-0207456P.
2000US-0234687P.
2000US-0236359P.
                                                  2001WO-US000661.
                                                                     2001WO-US000664
                                                                            2001WO-US000665.
                                           2000GB-00024263
                                                                                                                                                                                                                                                                                                                                                                                                             AGCTGGAGAACATGACG
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                                                                                                                                                                                                                                                                                                                                                                                       15; Conservative
                                                                                                                                            Ji Y, Penn SG,
                                                                                                                                                        WPI; 2002-179446/23.
                                                                                                                               (AEOM-) AEOMICA INC.
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                                                                     30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
                                                                                                      30-JAN-2001;
                                                                                                                   05-FEB-2001;
                                                  30-JAN-2001;
                                                              30-JAN-2001;
                                                                                                30-JAN-2001;
                                             04-OCT-2000;
                         26-MAY-2000;
                                     27-SEP-2000;
                                                                                                            30-JAN-2001
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                                                                                                                                           Gu Y,
                                                                                                                                                                                                                                                                                                                                                                                        Matches
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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates to hGDMLP-1 nucleic acids in samples, as amplification substrates to hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be consed as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption indisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The protein sequence senceding hGDMLP-1 may be used for diagnosing a clisorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence date for this patent did not form part of the printed continuous in the exemplification of the present invention. N.B. The special continuous conti
                                                                                                                                                                                                                                                                                      New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
Shannon ME;
Chen W,
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Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 13366; 214pp; English
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Hanzel DK,
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New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser descrption ionization, comprises human myosin-like protein hGDMLP-1.

Chen W, Shannon ME;

Hanzel DK, Rank DR,

Gu Y, Ji Y, Penn SG, WPI; 2002-179446/23.

(AEOM-) AEOMICA INC.

05-FEB-2001; 2001US-0266860P

30-JAN-2001;

2001WO-US000664 2001WO-US000665 2001WO-US000666 2001WO-US000667 2001WO-US000668 2001WO-US000669 2001WO-US000670

30-JAN-2001; 30-JAN-2001; 30-JAN-2001; 30-JAN-2001;

30-JAN-2001; 30-JAN-2001;

2000US-0236359P 2000GB-00024263 2001WO-US000662 2001WO-US000663

27-SEP-2000; 04-OCT-2000; 30-JAN-2001; 30-JAN-2001;

21-SEP-2000;

2001WO-US000661

25-MAY-2001; 2001WO-US016981

WO200192524-A2.

06-DEC-2001.

Homo sapiens

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-CC acids in gene therapy and vaccine production. The hGDMLP-1 concleic acids can be used as probes to detect, characterise and quantify chgMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 coprotein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP-1 proteins, as specific biomolecule capture probes for surface-enhanced laser describing in hGDMLP-1 coproduction, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The copulation sequence encoding hombLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart can askeletal muscle disorders. hGDMLP-1 may be used to chromosome 2.

The sequence data for this patent did not form part of the printed control of the printed 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25 BP; 8 A; 6 C; 9 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 13367; 214pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequence
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Best Local Similarity 88.2%
Best Local 15, Conservative
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Gaps

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(first entry)

29-MAY-2002

ABN13375;

3 AGCTGGAGAACATGACG 19

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The invention describes a dimer of a chimeric recombinant binding domain-
functional group fusion formed via disulfide-bond-bridge and a production
process thereof. The dimer has two times improved adhesion, and
excellently functions on a target. A dimer of chimeric recombinant
binding domain-functions on a target. A dimer of chimeric recombinant
consistency and proup (E) fusion is provided, wherein an extended
amino acid sequence (Ext) which is extended from the binding domain (B)
cot the function group (F) fuses the binding domain (B) and the functional
group (F); the extended amino acid sequence (Ext) contains cysteine
without an inner chain pair and forms disulfide-bond-bridge when the
contained between the last cysteine and the functional group (F); and
consists of flexible amino acid sequences of GASQEND, so that it can
decrease stearic hindrance between the functional group when the chimeric
recombinant binding domain(B)-functional group (F) fusion forms the
dimer. This sequence represents a primer associated with the chimeric
recombinant binding domain-functional group (F) fusion of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dimer of chimeric recombinant binding domain-functional group fusion formed via disulfide-bond-bridge and production process thereof.
                                                                                                                                                          dimer; chimeric recombinant binding domain-functional group fusion; steric hindrance; PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Won JS;
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                                                                                                                            Binding domain-functional group fusion related pRK primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25 BP; 1 A; 10 C; 9 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee YC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim YJ, Kwon HW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 25; 65pp; Korean.
               BP.
                                                                                                                                                                                                                                                                                                                                            30-JUN-2003; 2003KR-00043599
                                                                                                                                                                                                                                                                                                                                                                              29-JUN-2002; 2002KR-00037770
ADQ80648/c
ID ADQ80648 standard; DNA; 25
                                                                                         09-SEP-2004 (first entry)
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   (CHOE/) CHOE M H.
                                                                                                                                                                                                                                                               KR2004004095-A
                                                                                                                                                                                                                         Unidentified
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                                                     ADQ80648;
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Search completed: December 13, 2005, 13:34:17 Job time : 371.5 secs

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Indels

0; Mismatches

4 GCACAGCTGGGGAACAA 20

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GCGCGGCTGGGGAACAA

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Pasha, A.Q. and Ahsan, A.
Method of detecting predisposition to high altitude pulmonary edema
Patent: WO 2005047540-A 3 26-MAY-2005,
Council of Scientific and Industrial Research (IN)
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                                 Sequence 3
911 Synthetic
                                            AB067311 Syntheric
CQ628621 Sequence
CQ628623 Sequence
CQ628624 Sequence
CQ628625 Sequence
CQ628625 Sequence
CQ628625 Sequence
CQ628629 Sequence
AR469685 Sequence
AR469685 Sequence
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AR469689 Sequence
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AR469691 Sequence
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="Synthetic Oligonucleotide"
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Sequence 35 from Patent WO2005000888.
CQ979281.1 GI:57976534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other sequences; artificial sequences.
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CQ979281
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CQ979281 Sequence
AR071012 Sequence
AR090262 Sequence
CQ890345 Sequence
CQ896981 Sequence
AX58101 Sequence
AX68101 Sequence
CQ878645 Sequence
CQ878645 Sequence
CQ8718645 Sequence
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AR290163 Sequence
CQ623729 Sequence
AR464792 Sequence
AX673028 Sequence
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35 Surface p
                                                                                                                       December 13, 2005, 12:48:14; Search time 1116.5 Seconds (without alignments) 1221.892 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                        5883141 seqs, 28421725653 residues
                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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CQ979281
AR2901012
AR290145
CQ890345
CQ890345
AX642888
CQ878645
CQ878645
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CQ878645
CQ878645
CQ878645
AX487198
AR65235
AR673729
AR647323
AR647302
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Gapop 10.0 , Gapext 1.0
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Minimum DB Maximum DB

Database

Searched:

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Result Š

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Butz,K., Crnkovic-Mertens,I. and Hoppe-Seyler,F.D.
Livin-specific siRNAs for the treatment of therapy-resistant tumors
Patent: EP 1469070-A 1 20-OCT-2004;
Butsches Krebsforschungszentrum Stiftung des oeffentliche n Rechts
(DE)
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LIVIN-SPECIFIC siRNAS FOR THE TREATMENT OF THERAPY-RESISTANT TUMORS
Patent: WO 2004091388-A 1 28-OCT-2004;
Deutsches Krebsforschungszentrum Stiftung des oeffentliche n Rechts
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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93.8%; Pred. No. 7.7e+04;
tive 0; Mismatches 1;
                                                                                                 60.8%; Score 14.6; DB 6; ilarity 73.9%; Pred. No. 5.8e+04; Conservative 1; Mismatches 5;
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Sequence 1 from Patent WO2004091388.
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/organism="Home sapiens" |
/mol_type="unassigned RNA" |
/db_xref="taxon:9606"

    .19
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

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Sequence 1 from Patent EP1469070.
CQ890345
/organism="unknown"
/mol_type="genomic DNA"
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CQ896981.1 GI:55581823
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                                                                                                                                                                                                          /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_ref="taxon:32630"
/note="forward primer for amplifying beta-actin promoter containing intron 1"
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Cohen,D., Chumakov,I. and Blumenfeld,M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
Patent: US 6537751-A 1997 25-MAR-2003;
RRA;
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                                                 Bates, S.D. and Zhang, W.
Novel Beta-actin and RPS21 promoters and uses thereof
Patent: WO 2005000888-A 35 06-JAN-2005,
Genzyme Corporation (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 65.0%; Score 15.6; DB 6; Length 26; Best Local Similarity 81.8%; Pred. No. 1.9e+04; Matches 18; Conservative 0; Mismatches 4; Indels
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       other sequences; artificial sequences
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/mol_type="unassigned DNA"
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Sequence 13 from patent US 5910405.
AR071012
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Human p53 splice variant displaying differential transcriptional
activity
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Novel human p53 splice variant displaying differential
transcriptional activity
Patent: WO04008468-1A
Deppert, WOlfgang Willi (DE)
Location/Qualifiers
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Pred. No. 9.6e+04;
0; Mismatches 3;
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/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="pximer B11R"
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/mol_type="unassigned DNA"
/mol_type="taxon:32630"
/db_xref="taxon:32630"
/nofe="primer E11R"
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CQ890107
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other sequences, artificial sequences.
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other sequences; artificial sequences.
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Deppert, Wolfgang Willi (DE)
Location/Qualifiers
                                       CQ878645 21 bp
Sequence 17 from Patent EP1462521.
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CQ878645.1 GI:53791103
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Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
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           RESULT 9
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Method for the preferential nucleic acid synthesis reaction of one or more selected regions of one or more target nucleic acids
Patent: WO 02086155-A 7 31-0CT-2002;
LION Bioscience AG (DE)
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Method of blocking amplification of selected sequences
Patent: BP 1253205-A 7 30-OCT-2002;
LION Bioscience AG (DE)
Location/Qualifiers
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93.8%; Pred. No. 7.7e+04;
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60.0%; Score 14.4; DB 6;
Best Local Similarity 75.0%; Pred. No. 7.5e+04;
Matches 18; Conservative 0; Mismatches 6;

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    forganism="synthetic construct"
|mol_type="unassigned DNA"
|db_xref="taxon:32630"

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    .30
    /organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

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Sequence 7 from Patent W002086155.
AX642888 GI:28475108
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Sequence 7 from Patent EP1253205.
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Mus musculus
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synthetic construct
                                                          6 ACAGCTGGGGAACAAG
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           Best Local Similarity 93.8 Matches 15; Conservative
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PAT 21-JAN-2000

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unidentified
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1 (bases 1 to 37)
Chharwal,G.S. and Hammerschmidt,S.
Chharwal,G.S. and Hammerschmidt,S.
SURFACE PROTEIN (SPEA PROTEIN) OF STREPTOCOCCUS PNEUMONIAE, DELETED
BURILWATIVES, EXPRESSION SYSTEM FOR SAID PROTEINS AND VACCINE SYSTEM
WITH SAID PROTEINS
PATENT: WO 9819450.A 13 11-SEP-1998;
BIOTECHNOLOG FORSCHUNG GMBH (DE); CHHATWAL GURSHARAN SINGH (DE)
LOCATION/QUANIFIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Surface protein (SPsA protein) of streptococcus pneumoniae, deleted derivatives, expression system for said proteins and vaccine system BD082235
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58.3%; Score 14; DB 6; Length 37;
Best Local Similarity 77.3%; Pred. No. 1.2e+05;
Matches 17; Conservative 0; Mismatches 5; Indels
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77.3%; Pred. No. 1.2e+05;
iive 0; Mismatches 5;
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/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
                                                37 bp
Sequence 13 from Patent WO9839450.
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Neuralized protein, polynucleotide encoding said protein and antibody recognizing said protein

Patent: JP 1999137257-A 14 25-MAY-1999;
SUMITOMO ELECTRIC IND LTD
OS Unidentified

PD 25-MAY-1999
PP 14-NOV-1997 JP 1997313211
PR NOTOMI NAKADA, HIDEO NAKAMURA, MITSUHIRO YOSHIDA, HIDEYUKI SAYA
PC C12N15/09, C07K14/47, C07K16/18, C12P21/02, C12Q1/68, G01N33/53//PC C12N15/09, C12R1:91), (C12P21/02, C12R1:19), C12N15/00, (C12N15/00, PC C12R1:91)
CC Strandedness: Single;
CC Topology: Linear;
FH Key L. 23
FT Source L. 23
FT Source L. 23
FT F Source L. 23
FT Source L. 24
FT Source L. 25

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Candida albicans
Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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                                                                                                                              Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L. Gene disruption methodologies for drug target discovery Patent: WO 0205378-A 498 11-JUL-2002; Elitra Pharmaceuticals, Inc. (US) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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/organism='Unidentified'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14.2; DB 6;
Pred. No. 9.6e+04;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                       /organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"

    .23
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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JP 1999137257-A/14.
unidentified
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1 (bases 1 to 23)
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Best Local Similarity 84.2%;
Matches 16; Conservative (
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PAT 27-MAR-2003
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          PAT 20-FEB-2004
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Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
                                                                                                                                                                              Polynuclectide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle patent: US 6686188-A 8469 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
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88.2%; Pred. No. 1.5e+05;
iive 0; Mismatches 2; Indels
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Patent: WO 03004526-A 1473 16-JAN-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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17 bp DNA
Sequence 8469 from patent US 6686188.
AR464792.1 GI:42699849
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/mol_type="unassigned DNA"
/db xref="taxon:9606"
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Sequence 5 from patent US 6284463.
AR167144 GI:16243619
                                                                                                                                                                                                                                                                                                 /organism="unknown"
/mol_type="genomic DNA"
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AX673028/c
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Shannon,M.E.
                                                                                                                                                                                                                                   Unclassified.

1 (bases 1 to 47)

Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density disequilibrium map of the human genome Patent: US 6537751-A 1898 25-MAR-2003;
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Aeomica, Inc. (US)
Location/Qualifiers
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Pred. No. 1.2e+05;
1; Mismatches 1; Indels
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Sequence 1898 from patent US 6537751.
AR290163
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="unknown"
               22
                              12 GATCCACAGGCTGGAAACAAGA 33
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Best Local Similarity 87.5%;
Matches 14; Conservative 1
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AB067911.1 GI:15128715
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Matches 15; Conservative
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JP 2001321190-A/598
20-NOV-2001
12-NAR-2001
EIICHI SOEDA
CI2N15/09,CI2N15/09,CI2M1/00,CI2Q1/68,G01N33/53,G01N33/566,
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Patent: JP 2001321190-A 598 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
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/organism='Artificial Sequence'
Location/Qualifiers
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    forganism="synthetic construct"
|mol type="genomic DNA"
|db_xref="taxon:32630"

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102471
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synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 20)
                                        1 (bases 1 to 20)
Hasebe,M., Goto,M. and Tosu,M.
Method for detection of mutations
Patent: US 6284463-A 5 04-SEP-2001;
                                                                                                           1. .20
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A method of arraying genome clone.
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Matches 15; Conservative
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Synthetic construct DNA, reverse primer for human STS sts-F19245 at
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Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp, Tel:81-22-717-8047)
Location/Qualifiers
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1 (bases 1 to 20)
Bos J.L. and Van der Eb, A.J.
Probes and methods for detecting activated ras oncogenes
Patent: US 4871838-A 3 03-0CT-1989;
The Board of Rijks Universiteit Leiden; Leiden;
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1. .20
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Gaps

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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PAT 02-FEB-2004
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                             Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 13363 06-DEC-2001;
Aeomica, Inc. (US)
Location/Qualifiers
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Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 13364 06-DEC-2001;
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88.2%; Pred. No. 1.5e+05;
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Sequence 13365 from Patent WO0192524.
CQ628625 GI:41678843
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Sequence 13364 from Patent WO0192524.
CQ628624
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Location/Qualifiers
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae, Homo.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 13362 06-DEC-2001;
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Acomica, Inc. (US)
Location/Qualifiers
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CQ628621 25 bp DN Sequence 13361 from Patent WO0192524.

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VERSION KEYWORDS SOURCE ORGANISM

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
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Patent: WO 0192524-A 13368 06-DEC-2001;
                                                                                                                                 57.5%; Score 13.8; DB 6; Length 25; 88.2%; Pred. No. 1.5e+05; ive 0; Mismatches 2; Indels
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88.2%; Pred. No. 1.5e+05;
ive 0; Mismatches 2;
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/wol_type="unassigned DNA"
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Best Local Similarity 88.2
Matches 15; Conservative
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CQ628629
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Myosin-like gene expressed in human heart and muscle
Patent: WO 0192254-A 13367 06-DEC-2001;
            Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
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                                               Myosin-like gene expressed in human heart and muscle Patent: WO 0192524-A 13365 06-DEC-2001;
Acomica, Inc. (US)
Location/Qualifiers
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Patent: WO 0192524-A 13366 06-DEC-2001;
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Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2;
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Sequence 13367 from Patent WO0192524.
CQ628627
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Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle patent: US 6686188-A 13363 03-PBB-2004;
Amersham PLC; Buckinghamshire;
GBX;
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
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Sequence 13364 from patent US 6686188.
AR465687
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Sequence 13363 from patent US 6686188.
AR469686
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8 AGCTGGGGAACAAGACG 24
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AR469688
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AR469686
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
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                                            Query Match 57.5%; Score 13.8; DB 6; Length 25; Best Local Similarity 88.2%; Pred. No. 1.5e+05; Matches 15; Conservative 0; Mismatches 2; Indels
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Sequence 13361 from patent US 6686188.
AR469684
AR469684.1 GI:42704741
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Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle attent: US 6686188-A 13368 03-FBB-2004; Amersham PLC; Buckinghamshire; GBX;
 1 (bases 1 to 25)

Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle Patent: US 6686188-A 13367 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
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88.2%; Pred. No. 1.5e+05;
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ative 0; Mismatches 2;
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Best Local Similarity 88.44,
Best Local 15, Conservative
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Best Local Similarity 88.29
Matches 15; Conservative
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Shannon, M.E.
Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle parent: US 666188-A 13366 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;
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1 (bases 1 to 25)
Gu, Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
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57.5%; Score 13.8; DB 6;
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Matches 15; Conservative 0; Mismatches 2;
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Sequence 13365 from patent US 6686188. AR469688
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Sequence 13366 from patent US 6686188.
AR469689
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RESULT 37 AR469689

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Amersham PLC; Buckinghamshire; GBX;
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834656, 947795, 1574497,

Sequence

Sequence Sequence

Sequence 385942, Sequence 394642, Sequence 394667, Sequence 472467, Sequence 703352,

28079, 17960,

Sequence Sequence

Sequence

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Rhvorova, Anastasia
APPLICANT: Rkhvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Respuelds, Angela
APPLICANT: Respuelds, Stephen
APPLICANT: Marshall, William
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
SOFTWARE: POPPICATY
SOFTWARE: POPPICATY
SOFTWARE: POPPICATY
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US-10-770-726-27537

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US-10-770-726-27539

US-10-770-726-27999

US-10-770-726-28073

US-10-770-726-28074

US-10-770-726-28074

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US-110-770-726-28077

US-110-770-726-28077

US-110-770-726-28077

US-110-244-394642

US-111-101-244-394667

US-11-101-244-72467

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US-11-083-784-947800
; Sequence 947800, Application US/11083784
; Publication No. US2050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
. APPLICANT: Leake, Devin
. APPLICANT: Marshall, William
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Publication No. US20050246794A1
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Best Local Similarity 78.9
Matches 15; Conservative
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CORGANISM: Homo sapiens
US-11-101-244-947800
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     Sequence 248753,
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Sequence 332886,
Sequence 332886,
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                                                                                            December 13, 2005, 13:34:24 ; Search time 214.5 Seconds (without alignments) 41.830 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

2: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/USO1_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/USO1_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/USO1_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/USO1_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/USO1_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/USO1_NEW_PUB.seq:*
                   GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-11-083-784-947800
US-11-083-784-36342
US-11-083-784-36342
US-11-01-294-17050
US-11-01-294-647873
US-11-01-244-647873
US-11-101-244-647873
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US-11-101-244-36559
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US-11-101-244-36559
US-11-101-244-36553
US-11-101-244-36553
US-11-083-784-248753
US-11-083-784-170754
US-11-083-784-170754
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US-11-083-784-170754
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US-11-083-784-17174
US-11-083-784-17174
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                                                                                                                                                                                                                                             3392430 seqs, 186927314 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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24
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Match Length
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Length 19; Indels

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APPLICANT: Barany, Francis
APPLICANT: Furner, Daniel
APPLICANT: Pingle, Maneesh
APPLICANT: 19603/4121 (CRF D-2995-02)
CURRENT APPLICATION NUMBER: US/10/939,294A
CURRENT FILING DATE: 2004-09-10
PRIOR FILING DATE: 2003-09-12
NUMBER OF EQ ID NOS: 38895
SOFTWARE: PatentIn version 3.3
SEQ ID NO 17050
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                           APPLICANT: Scaring, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFRENCE: 1349908
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
FRIOR APPLICATION NUMBER: US/10/714,333
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: PROPRIECTOR
SEQ ID NOS: 1591911
SEQ ID NO 386342
LENGTH: 19
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84.2%; Pred. No. 6.5e+02;
ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.0%; Score 14.4; DB 9; Best Local Similarity 87.5%; Pred. No. 5.2e+02; Matches 14; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ), OTHER INFORMATION: oligonucleotide probe US-10-939-294A-17050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 17050, Application US/10939294A; Publication No. US20050266417A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-101-244-647873
; Sequence 647873 Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 GAGTGATGGCAAGCAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAGAGGCCAAGCAC 16
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              ) TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-386342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-10-939-294A-17050
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Sequence 346-342

Sequence 346-342

Sequence 346-342

Sublication No. USD050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Marchall, William
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-04-07

PRIOR FILING DATE: 2005-09-10

PRIOR PALICATION NUMBER: 60/426,137

PRIOR FLING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
FRICH APPLICATION NUMBER: US/10/714,333
FRICH APPLICATION NUMBER: 60/502,050
FRICH APPLICATION NUMBER: 60/502,050
FRICH FILING DATE: 2003-09-10
FRICH FILING DATE: 2003-09-10
FRICH FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 947800
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.8; DB 9;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Rhyorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 GGAGTGATGGCAAGCACGA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 78.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 GAGTGATGGCAAGCAC 21
                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
CORGANISM: Homo sapiens
US-11-083-784-947800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-11-101-244-386342
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US-11-083-784-386342
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LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                   Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Endemacon, Anaerasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Dowin
APPLICANT: Leake, Dowin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT APPLICATION NUMBER: US/10/714,333
PRIOR APLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PELING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 802569
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
CURRENT ELLING BATE: 2005-04-07
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 882569
LENGTH: 19
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Pred. No. 1.5e+03;
0; Mismatches 1;
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Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 882569, Application US/11083784 publication No. US20050245475A1 GENERAL INFORMATION:
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Best Local Similarity 93.3<sup>3</sup>
Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
CORGANISM: Homo sapiens
US-11-083-784-882569
                                                                                                                                                                                                                                                                 TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-882569
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US-11-101-244-248753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 19;
       APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 647873
                                                                                                                                                                                                                                                                                                                                                                2; Indels
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Pred. No. 9.7e+02;
1; Mismatches 2;
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Sequence 882569, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Rhyorova, Anastasia
APPLICANT: Reynolds, Angela
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Similarity 82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-11-083-784-647873
                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-11-101-244-647873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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Sequence 426653, Application US/11101244
Publication No. US2080246794A1
GENERAL INFORMATION:
APPLICANT: Charmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Beake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scalinge, Stephen
ITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-04-07
PRIOR PILING DATE: 2005-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 426653
LENGTH: 19
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                            APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.0%; Score 13.2; DB 8; Best Local Similarity 72.2%; Pred. No. 1.8e+03; Matches 13; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.2; DB 8;
Pred. No. 1.8e+03;
1; Mismatches 3;
                                                                                          CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: PROprietary
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 770754, Application US/11101244; Publication No. US20050246794A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GCGGAGTGATGGCAAGCA 20
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Reynolds, Angela
Leake, Devin
Marshall, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 55.0%;
Best Local Similarity 77.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anast
APPLICANT: Reynolds, Angel
APPLICANT: Laske, Devin
APPLICANT: Marshall, Willi
                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-11-101-244-341923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-426653
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i Sequence 287598, Application US/11101244

j Sequence 287598, Application US/11101244

j Publication No. US20050246794A1

j GENERAL INFORMATION:
    APPLICANT: Revorova, Anastasia
    APPLICANT: Revorova, Anastasia
    APPLICANT: Revorova, Anastasia
    APPLICANT: Revorova, Mastasia
    APPLICANT: Revorova, Mastasia
    APPLICANT: Revorova, Mastasia
    APPLICANT: Revorova, Milliam
    APPLICANT: Scaringe, Stephen
    TITLE OF INVENTION: Functional and Hyperfunctional siRNA
    FILE REFREERENT
    PRICATION NUMBER: 60/502,050
    PRIOR FILING DATE: 2005-04-07
    PRIOR FILING DATE: 2005-09-10
    PRIOR FILING DATE: 2005-09-10
    PRIOR FILING DATE: 2002-11-14
    NUMBER OF SEQ ID NOS: 1591911
    SOFTWARE: Proprietary
    SEQ ID NO 287598
    LENGTH: 19
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APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 08/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR PILIOR DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 248753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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Pred. No. 1.8e+03;
1; Mismatches 3;
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Sequence 341923, Application US/11101244; Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khovorova, Anastasia
APPLICANT: Reynolds, Angela
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Best Local Similarity 77.8
Matches 14; Conservative
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Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-11-101-244-248753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Homo sapiens
US-11-101-244-287598
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; Sequence 341923, Application US/11083784
; Publication No. USZO050245475A1
; GENERAL INFORMATION:
; APPLICANT: KNOXOVA, Anastasia
; APPLICANT: Reynold, Angela
; APPLICANT: Reynold, Angela
; APPLICANT: Respond, Angela
; APPLICANT: Beake, Devin
; APPLICANT: Beake, Devin
; APPLICANT: Scaringe, Stephen
; TITLE OF INVERTION: Functional and Hyperfunctional siRNA
; TITLE OF INVERTION: Punctional and Hyperfunctional siRNA
; TITLE OF INVERTION NUMBER: US/11/083,784
; CURRENT PILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; RIOR APPLICATION NUMBER: 60/502,050
; RRIOR FILING DATE: 2003-09-10
; RRIOR APPLICATION NUMBER: 60/502,050
; RRIOR APPLICATION NUMBER: 60/502,050
; RRIOR FILING DATE: 2003-09-10
; RRIOR PILING DATE: 2003-09-10
; RRIOR PILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SGPTWARE: Proprietary
; LENGTH: 10
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Pred. No. 1.8e+03;
2; Mismatches 3; Indels
                    APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
FRIOR APPLICATION NUMBER: US/10/714,333
FRIOR APPLICATION NUMBER: US/10/714,333
FRIOR APPLICATION NUMBER: 06/502,050
FRIOR FILING DATE: 2003-11-14
FRIOR APPLICATION NUMBER: 60/426,137
FRIOR APPLICATION NUMBER: 60/426,137
FRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 287598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
APPLICANT: Marshall, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
CRGANISM: Homo sapiens
US-11-083-784-287598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
ORGANISM: Homo sapiens
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US-11-083-784-426653
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| Sequence 248753, Application US/11083784
| Publication No. US20050245475A1
| GENERAL INFORMATION:
| APPLICANT: Dharmacon, Inc.
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Beake, Devin
| APPLICANT: Marshall, William
| APPLICANT: Marshall, William
| APPLICANT: MARSHIL, William
| APPLICANT: NUMBER: US/10/714,333
| PRIOR PLING DATE: 2003-11-14
| PRIOR PLING DATE: 2003-11-14
| PRIOR PLING DATE: 2003-11-14
| PRIOR FLING DATE: 2003-11-14
| NUMBER OF SEQ ID NOS: 1591911
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APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERBNCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR PLICATION NUMBER: 60/502,050
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 5002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 770754
LENGTH: 19
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Pred. No. 1.8e+03;
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Pred. No. 1.8e+03;
1; Mismatches 3;
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Sequence 287599, Application US/11083784

Publication No. US20050245475A1

SENERAL INFORMATTON:

APPLICANT: Bharmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens US-11-101-244-770754
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US-11-083-784-248753
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LENGTH: 19
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                                                                                                                                                                                                                                                                                                                         TYPE: RNA
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Barancis

APPLICANT: Dariel:

APPLICANT: Pingle, Manesh

TITLE OF INVENTION: Methods for identifying target nucleic acid molecules

FILE REFERENCE: 19603/4121 (CRF D-2995-02)

CURRENT APPLICATION NUMBER: US/10/939, 294A

FILE REFERENCE: 19603/4121 (CRF D-2995-02)

CURRENT APPLICATION NUMBER: US/09-09-10

PRIOR FILING DATE: 2004-09-12

NUMBER OF SEQ ID NOS: 38895

SOFTWARE: Patentin version 3.3

IENGTH: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CAGCGGAGTGATGGCAAG 18
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Best Local Similarity 83.34
Matches 15; Conservative
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Best Local Similarity 84.6
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-11-083-784-332886
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77.8%; Pred. No. 1.8e+03;
tive 1; Mismatches 3; Indels
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349908
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR FILING DATE: 2003-11-14
PRIOR PELICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-10-10
PRIOR PELICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 426653
LENGTH: 19
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US-11-083-794-770754

i Sequence 770754, Application US/11083784

j Publication No. US20550245475A1

i GENERAL INFORMATION:
    APPLICANT: Dharmacon, Inc.
    APPLICANT: Reynolds, Angela
    APPLICANT: Reynolds, Angela
    APPLICANT: Reynolds, Angela
    APPLICANT: Responds, Angela
    APPLICANT: Responds, Angela
    APPLICANT: Scaringe, Stephen
    TILL OF INVENTION: Functional and Hyperfunctional siRNA
    FILE FEFERENCE: 1349908.
    TURRENT APPLICATION NUMBER: US/11/083,784
    CURRENT FILING DATE: 2005-03-18
    FRIOR APPLICATION NUMBER: 60/502,050
    PRIOR FILING DATE: 2003-11-14
    PRIOR FILING DATE: 2003-11-14
    FRIOR FILING DATE: 2003-11-14
    NUMBER OF SEQ ID NOS: 1591911
    SOFTWARE: Proprietary
    SEQ ID NO 770754
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Pred. No. 1.8e+03;
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US-10-939-294A-17174
; Sequence 17174, Application US/10939294A
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Best Local Similarity 77.83
Matches 14, Conservative
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; ORGANISM: Homo sapiens
US-11-083-784-770754
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APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Rese, Devin
APPLICANT: Marshall, William
APPLICANTON Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349908
CURRENT APPLICATION NUMBER: US/11/101,244
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PLLING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NOS: 1591911
SEQ ID NOS: 1591911
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Pred. No. 2.2e+03;
2; Mismatches 0; Indels
                                                                                                                                       ; Sequence 332886, Application US/11101244; Publication No. US20050246794A1; GENERAL INFORMATION:
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B CAGCGGGGTGACGCGAG 25
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APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATIN
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: 108/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 27533
LENGTH: 21
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Sequence 27534, Application US/1077026

Publication No. US20050266409A1

GENERAL INFORMATION:

APPLICANT: Weeth

APPLICANT: Liu, Wei

APPLICANT: Liu, Wei

TITLE OF INVENTION:

TITLE OF INVENTION: CANCERS

FILE REFERENCE: AM101079 (031896-010000)

CURRENT APPLICATION NUMBER: US/10/770,726

CURRENT FILING DATE: 2004-02-04

NUMBER OF SEQ ID NOS: 48640

SOFTWARE: Patentin version 3.2

SEQ ID NO 25534

LENGTH: 21
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Pred. No. 2.3e+03;
2; Mismatches 0; Indels
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100.0%; Pred. No. 2.3e+03;
iive 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 27036
LENGTH: 21
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; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                 54.2%;
84.6%;
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.6'
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Best Local Similarity 84.6
Matches 11; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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; ORGANISM: RNAi
US-10-770-726-27534
                                                                                                                                                                                                                , ORGANISM: RNA1
US-10-770-726-27036
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US-10-770-726-27533
                                                                                                                                                                                             TYPE: RNA
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US-10-726-27036

US-10-770-126-27036

SQUENCE 27036

Publication No. US20050266409A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Liu, Wei

APPLICANT: Liu, Wei

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING

TITLE OF INVENTION: CANCERS

FILE REFERENCE: AM101079 (031896-010000)
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                                                                APPLICANT: Capital APPLICANT: Capital APPLICANT: Capital APPLICANT: Marshall, William APPLICANT: Marshall, William APPLICANT: Marshall, William APPLICANT: Scarible Functional and Hyperfunctional sirNA FILE REPERENCE: 13499US FILE REPERENCE: 13499US CURRENT APPLICATION NUMBER: US/11/083,784 CURRENT APPLICATION NUMBER: US/10/714,333 PRIOR FILING DATE: 2003-11-14 PRIOR APPLICATION NUMBER: 60/502,050 PRIOR FILING DATE: 2003-11-14 PRIOR PILING DATE: 2003-11-14 PRIOR FILING DATE: 2002-11-14 NUMBER OF SEQ ID NOS: 1591911 SEQ ID NO 332886 LENGTH: 19
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Pred. No. 2.3e+03;
0; Mismatches 0; Indels
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2.2e+03;
0;
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100.0%; Pre
                   Khvorova, Anastasia
                                             Reynolds, Angela
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4 GAGUGAUGGCAAG 16
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Best Local Similarity 100.
Matches 13; Conservative
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Matches 11; Conservative
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US-11-083-784-332886
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US-10-770-726-27035
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US-10-770-726-27035
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING; TITLE OF INVENTION: CANCERS; TITLE OF INVENTION: CANCERS; FILE REPERENCE: AM101079 (031896-010000); CURRENT APPLICATION NUMBER: US/10/770,726; CURRENT PILING DATE: 2004-02-04; NUMBER OF SEQ ID NOS: 48640 SOFTWARE: Patentin version 3.2 SEQ ID NO 27539 LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27989, Application US/10770726
Publication No. US20050266409A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Weth
APPLICANT: Liu, Weth
APPLICANT: Liu, Weth
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION UNDER: US/10/770.726
CURRENT PILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 27989
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Publication No. US20050266409A1

GENERAL INFORMATION:

APPLICANT: Brown, Eugene

APPLICANT: Liu, Wei

TITLE OF INVENTION: CANCERS

FILE REFERENCE: AM101079 (031896-010000)

CURRENT APPLICATION UNDER: US/10/770,726

CURRENT PILING DATE: 2004-02-04

NUMBER OF SEQ ID NOS: 48640

SOFTWARE: PREENTIN VERSION 3.2

SEQ ID NO 27990

LENGTH: 21
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Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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US-10-770-726-27539
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US-10-770-726-27989
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US-10-770-726-27989
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US-10-770-726-27990
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US-10-770-726-27990
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Publication No. US20050266409A1
EMBRAL INFORMATION:
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: CAMPGESITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANGERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: PALENTIN Version 3.2
SEQ ID NO 27536
LENGTH: 21
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APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
LENGTH: 21
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Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Brown, Bugene
                                                                                                                                             GAGTGATGGCAAG 18
                                                                                                                                                                                    5 GAGUGAUGGCAAG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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US-10-770-726-27539
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Publication No. US20050266409A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth,
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, TITLE OF INVENTION: CANDOSITIONS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION WUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
SEQ ID NO 28076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Publication No. US20050266409A1

GENERAL INFORMATION:
COMPANIENT:
Iniu, Weth
APPLICANT:
Iniu, Weth
TITLE OF INVENTION:
CURRENT APPLICATION WUMBER: US/10/770,726
CURRENT APPLICATION WUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: PATENTING PATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SEQ ID NO 28077
LENGTH: 21
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Publication No. US20050266409A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: CANCERS
TITLE OF INVENTION: CANCERS
TITLE OF INVENTION: CANCERS
TITLE OF INVENTION: CANCERS
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04

NUMBER OF SEQ ID NOS: 48640
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100.0%; Pred. No. 2.3e+03;
Live 0; Mismatches 0;
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Pred. No. 2.3e+03;
2; Mismatches 0
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SEQ ID NO 28079
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Best Local Similarity 84.6'
Matches 11; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
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; ORGANISM: RNAi
US-10-770-726-28077
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US-10-770-726-28079
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US-10-770-726-28077
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Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: CANCERS
FILE REFRENCE: AM101079 (031895-010000)
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
SEQ ID NO 28074
                                                                                                                                                                                                                                Sequence 28073, Application US/10770726

Publication No. US20050266409A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wyeth

APPLICANT: Liu, Wei

APPLICANT: Liu, Wei

APPLICANT: Liu, Wei

APPLICANT: APPLICANT: Liu, Wei

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING

TITLE OF INVENTION: CANCERS

FILE REFERENCE: AM 101079 (031896-010000)

CURRENT APPLICATION UNDERS: US/10/770,726

CURRENT APPLICATION UNDERS: 2004-02-04

NUMBER OF SEQ ID NOS: 48640

SOFTWARE: Patentin version 3.2

SEQ ID NO 28073

LENGTH: 21
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                                                                0; Indels
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Pred. No. 2.3e+03;
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Pred. No. 2.3e+03;
                            Score 13; DB 6; I
Pred. No. 2.3e+03;
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100.0%; Pred. No. -
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US-10-770-726-28076
; Sequence 28076, Application US/10770726
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84.6%;
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84.6%;
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Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                         6 GAGTGATGGCAAG 18
                                                                                                                             Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                Best Local Similarity 84.6
Matches 11, Conservative
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US-10-770-726-28073
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US-10-770-726-28074
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US-10-770-726-28074
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US-10-770-726-28073
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                                Query Match
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53.3%; Score 12.8; DB 8; Length 19; 81.2%; Pred. No. 2.8e+03;
                                             53.3%; Score 12.8; DB 8; Length 19; 75.0%; Pred. No. 2.8e+03; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                 General Inversations:
General Inversations:
General Inversations:
APPLICANT: Enhorova, Anastasia
APPLICANT: Reyrolds, Angela
APPLICANT: Resynolds, Angela
APPLICANT: Cack. Devin
APPLICANT: Rasinge, Stephen
APPLICANT: Marshall, William
APPLICANT: Marshall, William
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 394642
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Charmacon, Inc.
APPLICANT: Charmacon, Inc.
APPLICANT: Charmacon, Ansatasia
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
APPLICANT: Scaringe, Stephen
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANTON: Functional and Hyperfunctional siRNA
FILE REFRENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-01-14
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                                                                                                                                                                                                                                                                                                                 Sequence 394642, Application US/11101244 Publication No. US20050246794A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 GGAGTGATGGCAAGCA 20
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SOFWARE: Proprietary
SEQ ID NO 394667
LENGTH: 19
                                                                                                12; Conservative
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; ORGANISM: Homo sapiens
US-11-101-244-394642
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Matches 13; Conserv
                                             Query Match
Best Local Similarity
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US-11-101-244-394642
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US-11-101-244-394667
  US-11-101-244-385942
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US-10-939-294A-17960
Sequence 17960, Application US/10939294A
Sequence 17960, Application US/10939294A
PUBLICANT BARANTON:
APPLICANT BARANY, Francis
APPLICANT Fungle, Manesh
APPLICANT Fingle, Manesh
APPLICANT Fingle, Manesh
TILLE OF INVENTION: Methods for identifying target nucleic acid molecules
FILE REFERENCE: 19603/4121 (GRF D-2995-02)
CURRENT APPLICATION NUMBER: US/10/939,294A
CURRENT APPLICATION NUMBER: US/10/939,294A
PRIOR FILING DATE: 2004-09-10
PRIOR FILING DATE: 2004-09-12
SOFTWARE: PatentIn version 3.3
SEQ ID NO 17960

LENGTH: 32
TANDER OF SEQ ID NOS: 38895
SEQ ID NO 17960
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Sequence 385942, Application US/11101244

Sequence 385942, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Characon, Inc.
APPLICANT: Revorous, Anastasia
APPLICANT: Revolds, Angela
APPLICANT: Marchall, William
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TILE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
                                                                                                                     Query Match 54.2%; Score 13; DB 6; Length 21; Best Local Similarity 100.0%; Pred. No. 2.3e+03; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 54.2%; Score 13; DB 6; Length 32; Best Local Similarity 76.2%; Pred. No. 2.3e+03; Matches 16; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: oligonucleotide probe US-10-939-294A-17960
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                                                                                                                                                                                                                        6 GAGTGATGGCAAG 18
                                                                                                                                                                                                                                                    1 GAGTGATGGCAAG 13
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial
                                                                  US-10-770-726-28079
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Gaps



Sequence 8888, Ap Sequence 35, Appl Sequence 61599, Sequence 15256, A Sequence 15277, A Sequence 15277, A Sequence 15277, A Sequence 4241, Ap Sequence 4246, Ap Sequence 4498, Ap Sequence 3492, Ap Sequence 3492, Ap Sequence 3526, Ap Sequence 1927, Ap Sequence 1929, Ap

Sequence 4302, Sequence 4309,

ALIGNMENTS

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Sequence 4303, Application US/09780533A
Sequence 4303, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFRENCE: MRH800, 878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10713137
; Sequence 2, Application US/10713137
; Publication No. US20050106573A1
; GENERAL INFORMATION:
; APPLICANT: Pasha, Abdul Qadar Mohammad
; TITLE OF INVENTION: A method of detection of predisposition
; TITLE OF INVENTION: to high altitude pulmonary edema (HAPE)
; FILE REFERENCE: 09755-0018US1
; CURRENT APPLICATION UNDRER: US/10/713,137
; CURRENT FILING DATE: 2003-11-13
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 24; DB 9; Length 24; 100.0%; Pred. No. 0.15; 0; Indels ive 0; Mismatches 0; Indels
7 US-10-669-841-8888

9 US-10-182-049-35

10 US-11-719-956-607979

10 US-11-036-317-435997

7 US-10-138-674-15256

7 US-10-138-674-15256

7 US-10-287-949A-15256

7 US-10-287-949A-15277

7 US-10-712-672-4246

7 US-10-712-672-4246

7 US-10-712-672-435

8 US-09-780-533A-4335

3 US-09-727-046-3549

3 US-09-727-046-3549

3 US-09-727-046-3549

3 US-09-780-164-11817

3 US-09-780-164-11817

3 US-09-780-164-1810

10 US-11-060-756-248181

3 US-09-780-533A-4302

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Best Local Similarity 100.
Matches 24; Conservative
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             -09-780-533A-4303
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US-09-730-289B-2718
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Gaps

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Sequence 4389, Application US/10712672

Sequence 4389, Application US/10712672

Publication No. US20040102413A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaccuticals, Inc.

APPLICANT: Ribozyme Pharmaccuticals, Inc.

APPLICANT: Ribozyme Pharmaccuticals, Inc.

APPLICANT: Ribozyme Pharmaccuticals, Inc.

APPLICANT: Rewiggen, Jim

APPLICANT: McSwiggen, Jim

APPLICANT: McSwiggen, Jim

APPLICANT: McSwiggen, Jim

FILE REFERENCE: MBHB00-882-C (400/019)

CURRENT APPLICATION NUMBER: US/09/653,225

CURRENT FILING DATE: 2000-08-11

PRIOR PPLICATION NUMBER: 60/150,713

PRIOR APPLICATION NUMBER: 60/150,713

PRIOR FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 5586

SEQ ID NO 4389

SEQ ID NO 4389
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TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                    FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-1941
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                                                                                                                                                                                                                                                                                             Length 37;
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                                                                                                                                                                                                                                                                                         Query Match 71.7%; Score 17.2; DB 3; Best Local Similarity 77.3%; Pred. No. 2.7e+02; Matches 17; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 223011, Application US/11060756 Ubblication No. US20050221354A1 GENERAL INFORMATION:
APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AGCGGAGTGATGGCAAGCACGA 23
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                                                                                   TYPE: RNA
ORGANISM: Artificial Seguence
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin version 3.2
SEQ ID NO 223011
LENGTH: 25
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Matches 16; Conservative
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ORGANISM: probe
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US-10-712-672-4389
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                  SEQ ID NO 1941
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Publication No. US20030087847A1

GENERAL INFORMATION:

APPLICANT: Riboxyme Pharmaceuticals, Inc.

APPLICANT: Booher, Robert

APPLICANT: Holman, Patricia

APPLICANT: Fattaey, Ali

APPLICANT: Fattaey, Ali

APPLICANT: McSviggen, Jim

ITILE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK

TITLE OF INVENTION: Bazyme
                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-4303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enzymatic Nucleic Acid
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Sequence 2709, Application US/09730289B

Sequence 2709, Application US/09730289B

Sequence 2709, Application US/09730289B

Sequence 2709, Application US/09030050259AI

SEMERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: McSwiggen, Jim

TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease

FILE REPERENCE: MBHB00-864-A (400/006)

CURRENT APPLICATION NUMBER: US 60/169,100

PRIOR APPLICATION NUMBER: US 60/169,100

PRIOR FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 3897

SOFTWARE: PALENTING PARE: DATE: 
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71.7%; Score 17.2; DB 3; Length 37;
Best Local Similarity 77.3%; Pred. No. 2.7e+02;
Matches 17; Conservative 2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75.8%; Score 18.2; D
Best Local Similarity 78.3%; Pred. No. 90;
Matches 10; Conservative 2; Mismatches
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CURRENT APPLICATION NUMBER: US/09/776,474
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,983
PRIOR FILING DATE: 2000-02
NUMBER OF SEQ ID NOS: 2992
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CAGCGGAGTGATGGCAGGACGA 23
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PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
SEQ ID NO 4303
LENCTH: 37
                                                                                                                                                                                    TYPE: RNA ORGANISM: Artificial Seguence
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LENGTH: 37
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Matches
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Sequence 3502, Application US/09927046 Publication No. US20030064946A1 GENERAL INFORMATION:
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                  1 CAGCGGAGTGATGGCAAGCACGA 23
                                                          1 caececeucaucecauceacua 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Artificial Sequence
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US-09-780-533A-4266
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Sequence 2718, Application US/09730289B

Publication No. US20030050259A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, Jim

TITLE OF INTURITION: Method and Reagent for Treatment of Cardiac Disease

FILE RFERENCE: MBHB00-664-A (400/006)

CURRENT APPLICATION NUMBER: US 60/169,100

PRIOR APPLICATION UNMBER: US 60/169,100

PRIOR FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 3897

SOFTWARE: PATENTING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 3897
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APPLICANT: McSwiggen, Jim
APPLICANT: Chowile, Bharat
APPLICANT: Chowile, Bharat
APPLICANT: Haeberli, Pete
TILE NEFERENCE: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBHB00, 878-A (400/011)
CURRENT APPLICATION NUMBER: U5/09/780, 533A
CURRENT FILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-02-11
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                                       69.2%; Score 16.6; DB 10; Length 25; 82.6%; Pred. No. 5.3e+02; ive 0; Mismatches 4; Indels
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69.2%; Score 16.6; DB 3;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4;
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Pred. No. 5.3e+02;
2; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CAGCGGAGTGATGGCAAGCACGA 23
                                                                                                                                  2 AGCGGAGTGATGCCAAGCACGAC 24
                                                                                                                                                                AGCGGAGTGACAGTAAGCAGGAC 24
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SOFTWARE: Patentin version 3.0
SEQ ID NO 4266
LENGTH: 37
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ORGANISM: Artificial Sequence
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                                                                 Best Local Similarity 82.6
Matches 19; Conservative
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Best Local Similarity 73.9
Matches 17; Conservative
US-11-060-756-223011
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US-09-780-533A-4266
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US-09-730-289B-2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2718
LENGTH: 37
                                              Query Match
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DEFLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McKenzie, Jim
APPLICANT: McKenzie, Tim
APPLICANT: Ayers, Dave
APPLICANT: Szymkowski, Edmund
APPLICANT: Szymkowski, Edmund
TITLE OF INVENTION: Channel-1
FILE REFERENCE: 249/021
CURRENT APPLICATION NUMBER: US/09/927,046
CURRENT APPLICATION NUMBER: US/09-09
NUMBER OF SEQ ID NOS: 5450
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3502
LENGTH: 37
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APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Mcxfagen, Jim
APPLICANT: Mcxfager, Jim
APPLICANT: Mcxfager, Jim
APPLICANT: Mcxfager, Dava
TILE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBHB00-845-H (400/029)
CURRENT APPLICATION NUMBER: US/09/877,478
CURRENT FILING DATE: 2001-12-31
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR PLING DATE: 2000-08-09
PRIOR PLING DATE: 2000-08-09
PRIOR PLING DATE: 2000-08-09
PRIOR PLING DATE: 1994-02-07
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1995-05-04
PRIOR PLING DATE: 1995-05-04
PRIOR PLING DATE: 1995-05-04
PRIOR PLING DATE: 1995-05-04
PRIOR PLING DATE: 1995-11-08
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69.2%; Score 16.6; DB 3;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4;
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Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
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Gaps

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RESULT 13
US-09-930-423-2765
i Sequence 2765, Application US/09930423
j Sequence 2765, Application US/09930423
g GENERAL INFORMATION:
j APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REPERENCE: MBHB00, 318-A 400/027
CURRENT APPLICATION NUMBER: US/09/930, 423
CURRENT PILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 4553
SOFTWARE: Patentin version 3.0
LENGTH: 37
LENGTH: 37
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APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: MBHB00, 918-A 400/027
CURRENT PLILIG DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 4553
SOFTWARE Patentin version 3.0
SEQ ID NO 2786
LENGTH: 37
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69.2%; Score 16.6; DB 3;
Best Local Similarity 73.9%; Pred. No. 5.38+02;
Matches 17; Conservative 2; Mismatches 4;
  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2786, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
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  2;
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ORGANISM: Artificial Sequence
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  17; Conservative
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US-09-745-237A-2746
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US-09-930-423-2786
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    Matches
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APPLICANT: Blatt, Larry
APPLICANT: MCSAviggen, Jim
TITLE OF INVENTION: Mcthod and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: Method, 918-A 400/027
CURRENT APPLICATION WUMBER: US/09/930, 423
CURRENT FILING DATE: 201-08-15
NUMBER OF SEQ ID NOS: 4553
SOFTWARE: Patentin version 3.0
SEQ ID NO 2746
LENGTH: 37
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US-09-930-423-2746
                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
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                                                                                                                                                                                         Query Match
69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels
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. OTHER INFORMATION: Description of Artificial Sequence:
05-09-330-423-2764
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Pred. No. 5.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                      US-09-930-423-2746

Sequence 2746, Application US/09930423

Publication No. US20030092003A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                     1 CAGCGGAGTGATGGCAAGCACGA 23
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SOFTWARE: Patentin version 3.0 SEQ ID NO 4013 LENGTH: 37
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                                                                                   ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
                                                                                                                                               US-09-877-478-4013
                                                                  TYPE: RNA
                                                                                                         FEATURE:
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Query Match
Best Local Similarity
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US-09-745-237A-2786
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LENGTH: 37
                                                                      FEATURE:
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Sequence 2754, Application US/09045237A

Publication No. US20030143708A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REPRENCE: 400/007 (WHHB00-918-A)
CURRENT APPLICATION NUMBER: US/09/745,237A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SECHWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TILLE OF INVENTION: McSwiggen, Jim
TILLE OF INVENTION: McHod and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: 400/007 (MBHB00.918-A)
CURRENT APPLICATION NUMBER: US/09/745,237A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-745-237A-2764
                                             APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REPERENCE: 400/007 (MBHB00-918-A)
FILE REPERENCE: 400/007 (MBHB00-918-A)
CURRENT APPLICATION NUMBER: US/09/745,237A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2746
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                      FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bnzymatic Nucleic Acid
US-09-745-237A-2746
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 69.2%; Score 16.6; DB 3; Best Local Similarity 73.9%; Pred. No. 5.3e+02; Matches 17; Conservative 2; Mismatches 4;
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69.2%; Score 16.6; DB 3;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4;
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                           APPLICANT: Ribozyme Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CGGCGGCGUGAUGGCAUGCACUA 23
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US-09-745-237A-2765
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                                                                                                                                                                                                                                                                                                TYPE: RNA
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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Wordsen, US/10/342,902
CURRENT APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2000-08-03-20
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-08-03-20
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1992-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
TITLE OF INVENTIVO: McHebod and Reagent for the Treatment of Alzheimer's Disease
FILE REPERENCE: 400/007 (MBHB00-918-A)
CURRENT APPLICATION NUMBER: US/09/745,237A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2786
LENGTH: 37
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US-09-745-237A-2786
                                          ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-09-745-237A-2765
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                                                                                                                        69.2%; Score 16.6; DB 3; Length 37; llarity 73.9%; Pred. No. 5.3e+02; Conservative 2; Mismatches 4; Indels
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Pred. No. 5.3e+02;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2786, Application US/09745237A; Publication No. US20030143708A1; GENERAL INFORMATION: APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 4013, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
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Best Local Similarity 73.9°
Matches 17; Conservative
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y APPLICANT: Ribozyme Pharmaceuticals, Inc.,
APPLICANT: Blatt, Larry
APPLICANT: Moxidsey, Jave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBHEO-845-41 (400/029)
CURRENT APPLICATION NUMBER: US/09/877,478
CURRENT APPLICATION NUMBER: US 07/882,712
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR APPLICATION NUMBER: US 09/536,385
PRIOR FILING DATE: 2000-03-20
PRIOR PILING DATE: 2000-03-09
PRIOR PLING DATE: 2000-10-09
PRIOR PLING DATE: 2000-10-07
PRIOR APPLICATION NUMBER: US 08/636,347
PRIOR APPLICATION NUMBER: US 08/434,504
PRIOR FILING DATE: 1994-02-07
PRIOR PELING DATE: 1995-05-04
PRIOR PLING DATE: 1995-05-04
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1999-110 NUMBER: US 08/436,430
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APPLICANT: Ribozymalicus;
APPLICANT: Ribozymalicus;
APPLICANT: Blatt, Larry
APPLICANT: Blatt, Larry
APPLICANT: Chowring, Jim
APPLICANT: Chowring, Dim
APPLICANT: Haeberli, Pete
TITLE OF INVENTION Method and Reagent for the Inhibition of NOGO Gene;
TITLE OF INVENTION MABER: US/09/780,533A
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT APPLICATION NUMBER: US 60/181,797
PRIOR APPLICATION NUMBER: US 60/181,797
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4274
   Gaps
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Pred. No. 8.3e+02;
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76.2%; Pred. No. b...
2; Mismatches
      2; Mismatches
                                                                                                                                                                                                                                                                                      Sequence 4274, Application US/09780533A publication No. US20030060611A1 GENERAL INFORMATION:
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Matches 16, Conservative
      17; Conservative
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US-09-780-533A-4274
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APPLICANT: Renneth, Disper
APPLICANT: Renneth, Disper
APPLICANT: Renneth, Disper
APPLICANT: Renneth, Disper
APPLICANT: Colisabeth, Roberts
TITLE OF INVENTION: VIRON REPLICATION
TITLE OF INVENTION: VIRON REPLICATION
FILE REPRENCE: 400/04208 (MBH02-249-E)
CURRENT APPLICATION NUMBER: US/10/669, 841
CURRENT PILING DATE: 2003-09-23
FRICH APPLICATION NUMBER: US 60/296, 876
FRICH APPLICATION NUMBER: US 60/296, 876
FRICH RELING DATE: 2001-06-08
FRICH RELING DATE: 2001-06-08
FRICH RELING DATE: 2001-06-08
FRICH RELING DATE: 2001-06-08
FRICH RELING DATE: 2001-03-05
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FRICH RELING DATE: 2000-03-11
FRICH RELING DATE: 2000-03-15
FRICH RELI
                                                                                                                                                                                                                                                          FEATURE:
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-342-902-4013
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US-10-669-841-8904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Score 16.6; DB 7;
Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
PRIOR APPLICATION NUMBER: US 09/436,430 PRIOR FILING DATE: 1999-11-08 NUMBER OF SEQ ID NOS: 6592 SCPTWARE: Patentin version 3.2 SEQ ID NO 4013 LENGTH: 37
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Publication No. US20040127446A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Lawrence, Blatt
APPLICANT: Dennis, Macejak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAGCGGAGTGATGGCAAGCACGA 23
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73.9%;
                                                                                                                                                                                                    TYPE: RNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                           Match 69.2%;
Local Similarity 73.9%;
es 17; Conservative
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David, Morrissey
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Best Local Similarity
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LENGTH: 37
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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ORGANISM: Artificial Sequence
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                                                            David, Morrissey
James, McSwiggen
                                                                                                                                                                          Patrice, Lee
Kenneth, Draper
                                                                                                                   Pamela, Pavco
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| Sequence 3997, Application US/10342902
| Sequence 3997, Application US/10342902
| Publication No. US20040054156A1
| GENERAL INFORMATION:
| APPLICANT: Sirna Therapeutics, Inc. |
| APPLICANT: Darger, Remneth |
| APPLICANT: Darger, Larry |
| APPLICANT: Morrissey, Dave |
| TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication |
| FILE REFERENCE: 400/075 (MBHB00-845-1) |
| CURRENT PILING DATE: 2003-01-15 |
| CURRENT PILING DATE: 2001-0-6-08 |
| PRIOR PLICATION NUMBER: US 09/531,025 |
| PRIOR PLICATION NUMBER: US 09/531,025 |
| PRIOR PLICATION NUMBER: US 09/531,025 |
| PRIOR PLICATION NUMBER: US 09/536,347 |
| PRIOR PLICATION NUMBER: US 09/696,347 |
| PRIOR PLICATION NUMBER: US 09/696,347 |
| PRIOR PLICATION NUMBER: US 09/696,347 |
| PRIOR PLICATION NUMBER: US 09/436,430 |
| PRIOR PLICATION UNMER: US 09/436,4
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US-09-877-478-3997
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US-10-669-841-8888
S. Sequence 8888, Application US/10669841
Publication No. US20040127446A1
GENERAL INFORMATION:
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      SOFTWARE: PatentIn version 3.0 SEQ ID NO 3997 LENGTH: 37
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Best Local Similarity 76.2
Matches 16; Conservative
                                                                                                                                                                                                  TYPE: RNA
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APPLICANT: Semala, Bracca
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APPLICANT: Memala, Bracca
APPLICANT: Memala, Bracca
APPLICANT: Memala, Proper
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Publication No. US20040077565A1
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TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERENCE: 365-01
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR PELING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NOS: 991174
SEQ ID NOS: 991774
SEQ ID NOS: 991774
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                                                                                                                                                                                                                                                                                                  APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 35.71
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR PILING DATE: 2002 11 20
PRIOR PILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 607979
LENGTH: 25
                                   66.7%; Score 16; DB 9; Length 18; 100.0%; Pred. No. 1e+03; ive 0; Mismatches 0; Indels
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1e+03;
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Pred. No. 1
                                                                                                                                                                                                                                           Sequence 607979, Application US/10719956 Publication No. US20040146910A1 GENERAL INFORMATION:
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US-11-036-317-435997
; Sequence 415997, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
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US-10-138-674-15256
; Sequence 15256, Application US/10138674
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Best Local Similarity 79.2%;
Matches 19; Conservative 6
                                                                                                              9 TGATGGCAAGCACGAC 24
                                                                                                                                    18 TGATGCCAAGCACGAC 3
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                                 Query Match
Best Local Similarity 100.0
Matches 16; Conservative
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US-11-036-317-435997
                                                                                                                                                                                                           RESULT 26
US-10-719-956-607979/c
US-10-182-049-35
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GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Bayco, Pam

APPLICANT: Bayco, Pam

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Jaime

APPLICANT: Stinchcomb, Jaime

APPLICANT: Stinchcomb, Jaime

APPLICANT: Stinchcomb, Dan

APPLICANT:
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Publication No. US20040077565A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Bacobed, Jam

APPLICANT: Stinchcomb, Dan

APPLICANT: Bacobed, Jaime

APPLICANT: Bacobed, Jaime

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels US/10/138,674

CURRENT APPLICATION NUMBER: US/10/138,674

CURRENT FILING DATE: 2002-05-03

SOFTWARE: PatentIn version 3.0

SEQ ID NO 15277

LENGTH: 36

LENGTH: 36
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Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2;
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Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.,
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
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US-10-712-672-4246

US-10-712-672-4246

Sequence 4246, Application US/10712672

Publication No. US20040102413A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Chowrira, Bharat
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McHood and Reagent for the Inhibition of Telomerase Enzyme
ITITE OF INVENTION: Whethod and Reagent for the Inhibition of Telomerase Enzyme
FILE REFERENCE: MBHB00-882-C (400/019)
CURRENT APPLICATION NUMBER: US/99/653,225
FRIOR APPLICATION NUMBER: 60/197,769
FRIOR FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/150,713
FRIOR APPLICATION NUMBER: 60/150,713
FRIOR APPLICATION NUMBER: 60/150,713
FRIOR FILING DATE: 1999-08-31
FRIOR APPLICATION NUMBER: 60/150,713
FRIOR APPLICATION NUMBER: 60/150,713
FRIOR APPLICATION NUMBER: 60/144
FRIOR FILING DATE: 1999-08-31
FRIOR APPLICATION NUMBER: 60/150,713
FRIOR APPLICATION NUMBER: 60/150,713
FRIOR APPLICATION NUMBER: 60/150,713
FRIOR FILING DATE: 1999-08-31
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US-10-712-672-4241
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TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Publication No. US20040102413A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
PRIOR APPLICATION NUMBER: 2000-08-31
PRIOR PILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/197,769
PRIOR PILING DATE: 2000-04-14
PRIOR PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 5586
SOFTWARE: Patentin version 3.0
SEQ ID NO 4241
LENGTH: 36
         APPLICATION NUMBER: US/09/653,225
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APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
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Matches 15; Conservative
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Best Local Similarity
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US-10-712-672-4375
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                                           APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REPERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NGS: 20822
SOFTWARE: Patent In version 3.0
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US-10-287-949A-15277
                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-10-287-949A-15256
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APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: McHood and Reagent for the Inhibition of Telomerase Enzyme
FILE REFERENCE: MBHB00-882-C (400/019)
CURRENT APPLICATION NUMBER: US/10/712,672
CURRENT FILING DATE: 2003-11-13
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APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Cor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287, 949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
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Pred. No. 1.3e+03;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.8; DB 7;
Pred. No. 1.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ribozyme Pharmaceuticals, Inc. APPLICANT: Pavco, Pam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15277, Application US/10287949A Publication No. US20040102389A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 GGAGTGATGGCAAGCACGA 23
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78.9%;
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ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                  TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 78.9°
Matches 15, Conservative
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Matches 15; Conservative
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US-10-287-949A-15277
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LENGTH: 36
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LENGTH: 36
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APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: Thompson, Jim
APPLICANT: Thompson, Jim
APPLICANT: Thompson, Jim
APPLICANT: Ayers, Dave
APPLICANT: Szymkowski, Edmund
ITILE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
TITLE OF INVENTION: Channel-1
FILE REFERENCE: 249/021
                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-4335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-09-927-046-3492
                         APPLICANT: Chowrira, Bharat
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBHBOOL, 878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT APPLICATION NUMBER: US 60/181,797
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SEQ ID NO 4335
LENGTH: 37
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Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.8; DB 3;
Pred. No. 1.3e+03;
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78.3%; Pred. No. 1...
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CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 5450
SOFTWARE: Patentin version 3.0
SEQ ID NO 3492
LENGTH: 37
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Sequence 3526, Application US/09927046
Publication No. US20030064946A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McKenzie, Tim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3492, Application US/09927046; Publication No. US20030064946A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                       TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 78.9
Matches 15; Conservative
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Publication No. US20040102413A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: APPLICANT: Acsignen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: APPLICANTON NUMBER: US/09/619)
CURRENT PILING DATE: 2003-11-13
PRIOR PRIOR PLING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 5586
SEQ ID NO 4498
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-712-672-4375
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US-10-712-672-4498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 36;
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                 CURRENT APPLICATION NUMBER: US/10/712,672
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: US/09/653,225
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 5586
SOFTWARE: Patentin version 3.0
SERIORHARE: 3475
LENGTH: 36
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; Sequence 4335, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.; APPLICANT: Blatt, Larry
FILE REFERENCE: MBHB00-882-C (400/019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGAGUGAUGCCAUGCACUA 20
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US-10-712-672-4498
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Gaps

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Page 11

APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (C:
TITLE OF INVENTION: Bn2yme
TITLE OF INVENTION: Bn2yme
FILE REFERENCE: MBHB00-955-A (400/008)
CURRENT APLICATION NUMBER: US (90/776, 474
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179, 983
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 2992
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1927
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid US-09-776-474-1927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 65.8%; Score 15.8; DB 3; Length 37; Best Local Similarity 78.9%; Pred. No. 1.3e+03; Matches 15; Conservative 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
ORGANISM: Artificial Sequence
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APPLICANT: Grupe, Andrew
APPLICANT: Grupe, Andrew
APPLICANT: Symkowski, Edmund
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
TITLE OF INVENTION: Channel-1
FILE REPERENCE: 249/021
CURRENT APPLICATION NUMBER: US/09/927,046
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 5450
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3549
LENGIN: 37
TYPE
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APPLICANT: Grupe, Andrew
APPLICANT: Grupe, Andrew
APPLICANT: Grupe, Andrew
APPLICANT: Szymkowski, Edmund
APPLICANT: Szymkowski, Edmund
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
TITLE OF INVENTION: Channel-1
FILE REPERENCE: 249/021
CURRENT APPLICATION NUMBER: US/09/927,046
CURRENT APPLICATION NUMBER: US/09-09
NUMBER OF SEQ ID NOS: 5450
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3526
LENGTH: 37
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CTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-927-046-3549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-09-927-046-3526
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APPLICANT: Jarvis, Thale
APPLICANT: Booher, Robert
APPLICANT: Holman, Patricia
APPLICANT: Fattaey, Ali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3549, Application US/09927046
Publication No. US20030064946A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: McSwiggen, Jim
APPLICANT: Thompson, Jim
APPLICANT: McKenzie, Tim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1927, Application US/09776474; Publication No. US20030087847A1; GENERAL INFORMATION:
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RESULT 2
US-09-371-772B-13000
; Sequence 13000, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.; APPLICANT: Pavco, Pam
; APPLICANT: Stinchcomb, Jim
; APPLICANT: Stinchcomb, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGUGAUGGCAUGCACUA 20
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Sequence 12711, A
Sequence 12725, A
Sequence 14177, A
Sequence 825, App
Sequence 1014, Ap
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            825, App
1014, Ap
1012, Ap
4012, Ap
4013, Ap
4014, Ap
4016, Ap
4016, Ap
4018, Ap
11279, Ap
11279, Ap
11279, Ap
11373, Ap
12964, Ap
12964, Ap
12964, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12979, A
Sequence 13000, A
                                                                                                (without alignments)
408.244 Million cell updates/sec
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                                                                                   December 13, 2005, 13:14:34 ; Search time 104.5 Seconds
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Sequence 5
Sequence 1
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Sequence
Sequence
Sequence
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(cgn2_6/ptodata/1/ina/5_COMB.seq:*

(cgn2_6/ptodata/1/ina/5_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/H_COMB.seq:*

(cgn2_6/ptodata/1/ina/PP_COMB.seq:*

(cgn2_6/ptodata/1/ina/PP_COMB.seq:*

(cgn2_6/ptodata/1/ina/PP_COMB.seq:*

(cgn2_6/ptodata/1/ina/PP_COMB.seq:*

(cgn2_6/ptodata/1/ina/PP_COMB.seq:*

(cgn2_6/ptodata/1/ina/PP_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-371-772B-13000
US-09-371-772B-13010
US-09-371-772B-12711
US-09-371-772B-14270
US-09-371-772B-14270
US-09-371-772B-14270
US-09-479-005A-1014
US-09-479-005A-1014
US-09-479-005A-1014
US-09-866-108A-4012
US-09-866-108A-4013
US-09-866-108A-4014
US-09-866-108A-4016
US-09-866-108A-4016
US-09-866-108A-4016
US-09-866-108A-4017
US-09-866-108A-4017
US-09-866-108A-4017
US-09-866-108A-4019
US-09-866-108A-4019
US-09-371-772B-12719
US-09-371-772B-12719
US-09-371-772B-12719
US-09-371-772B-12719
US-09-371-772B-12719
US-09-371-772B-13713
US-09-371-772B-13719
US-09-371-772B-13173
US-09-371-772B-13173
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Maximum Match 100%
Listing first 45 summaries
                                                       - nucleic search, using sw model
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24
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Match Length
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US-UJ-371-772B-12979
; Sequence 12979, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Baco, Pam
; APPLICANT: Bacobedo, Jaime
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions I
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION NUMBER: US 60/005,974
; FRIOR TILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR APPLICATION NUMBER: US 68/584,040
; RIOR DATE: 1996-01-08
; SEQ ID NO 12979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12979
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     14162, A
665, App
785, App
938, App
42756, A
                                                                                                                               Sequence 12754, Sequence 12767, Sequence 12819, Sequence 12890, Sequence 12939, Sequence 12978, Sequence 13014, Sequence 13065, Sequence 13065,
                                                                                                                                                                                                                                                                                                                           13067
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                                                                 Sequence 42
Patent No. 5
Sequence 12
                     Sequence
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US-09-371-772B-14162
US-09-479-005A-665
US-09-479-005A-785
US-09-3796-196G-42756
S519127-6
US-09-371-772B-12724
US-09-371-772B-12724
US-09-371-772B-12764
US-09-371-772B-12764
US-09-371-772B-12819
US-09-371-772B-12819
US-09-371-772B-12919
US-09-371-772B-12919
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US-09-371-772B-12978
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US-09-371-772B-13978
US-09-371-772B-13978
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US-09-371-772B-13978
US-09-371-772B-13065
US-09-371-772B-13065
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
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Best Local Similarity
Matches 15; Conserv
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APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
FILE REPERENCE: MBHB00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,72B
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12711
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Bescobedo, Jaine
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R:
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00, 876-J (237/198)
CURRENT FILING DATE: 1999-08-10
PRIOR PELING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ 1D NOS: 14225
SOFFWARE: PatentIn version 3.0
SEQ 1D NO 12725
LENTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-09-371-7728-12711
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US-09-371-772B-12725
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Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
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US-09-371-772B-14177
; Sequence 14177, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 75.04
Matches 15; Conservative
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US-09-371-772B-12725
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                          TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re FILE REFERENCE: Mahenous 16-J (237/198)
FILE REFERENCE: Mahenous 16-J (237/198)
CURRENT PELLING UNMER: US 60/005,974
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR PAPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ 1D NOS: 14225
SOFTWARE: PatentIn version 3.0
LENGTH: 36
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US-09-371-772B-13000
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US-09-479-005A-597
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| Sequence 597, Application US/09479005A
| Patent No. 6656731
| GENERAL INFORMATION:
| APPLICANT: Ribozyme Pharmaceuticals, Inc.
| TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
| FILE REFRENCE: MBHB00-884-C
| CURRENT APPLICATION NUMBER: US/09/479,005A
| CURRENT FILING DATE: 1999-11-19
| PRIOR PILING DATE: 1998-11-19
| PRIOR FILING DATE: 1998-09-22
| PRIOR FILING DATE: 1998-09-22
| NUMBER OF SEQ ID NOS: 1208
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 597
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; Sequence 12711, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: Stockaygen, Jim
; APPLICANT: StinchComb, Dan
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           Escobedo, Jaime
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; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-479-005A-825
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US-09-479-005A-1014
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FILE REFERENCE: MBHB00-884-C
CURRENT APPLICATION NUMBER: US/09/479,005A
CURRENT FILING DATE: 2000-01-07
FRIOR PILING DATE: 1999-11-19
FRIOR PILING DATE: 1999-10-29
FRIOR PILING DATE: 1999-09-22
FRIOR FILING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 1208
SOFTWARE: PATCHTON NUMBER: US 60/059,473
FRIOR FILING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 1208
SEQ ID NO 1014
                 APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFERENCE: MBHB00-884-C
CURRENT FILING DATE: 1050-61-07
PRIOR PLILNG DATE: 2000-01-07
PRIOR PLILNG DATE: 1999-11-19
PRIOR PLILNG DATE: 1999-11-19
PRIOR PLILNG DATE: 1999-09-22
PRIOR PLILNG DATE: 1998-09-22
PRIOR PLILNG DATE: 1997-09-22
PRIOR PLILNG DATE: 1997-09-22
PRIOR PLILNG DATE: 1997-09-22
PRIOR PLILNG DATE: 1997-09-22
SPRIOR PLILNG DATE: 1997-09-22
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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; Patent No. 6521425
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: RNA
ORGANISM: Artificial Sequence
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APPLICANT: Perler, Francine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 75.0
Matches 15; Conservative
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Best Local Similarity '
    GENERAL INFORMATION:
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Sequence 14200, Application US/09371772B

Patent No. 6566127

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bacobedo, Dam
APPLICANT: Stinchcomb, Dam
APPLICANT: Stinchcomb, Dam
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels 06 Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: WHORER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR PLILNG DATE: 1995-10-26
PRIOR PLILNG DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
SOFTWARE: PatentIn version 3.0
SEQ ID NOS: 14225
SEQ ID NO 14200
LENGTH: 36
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Estinchcomb, Dan
APPLICANT: Estinchcomb, Dan
APPLICANT: Estinchcomb, Dan
APPLICANT: Estinchcomb, Dan
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
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US-09-371-772B-14200
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US-09-371-772B-14177
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Pred. No. 8.3e+02;
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75.0%; Pred. No. 6...
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 75.0
Matches 15, Conservative
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Best Local Similarity
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US-09-479-005A-825
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APPLICANT: CHEN, Wencheng K.

APPLICANT: CHEN, Wencheng K.

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: WAOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERBNCE: AECMICA-7

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/206-26

PRIOR PILING DATE: 2000-10-4

PRIOR PILING DATE: 2000-10-4

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30
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NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 666188
SEQ ID NO 4013
LENGTH: 25
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88.9%; Pred. No. 1.2e+03;
Mismatches
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APPLICANT: GU, Yizhong APPLICANT: T. Yonggang APPLICANT: PENN, Sharron G. APPLICANT: HANZEL, David K.
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                                                            5 GGAGTGATGGCAAGCACG 22
                                                                                                                                GGAGTGAAGGGAAGCACG 25
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                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: GI, Yongang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: CHEN, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGTGAAGGGAAGCACG
Conservative
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Matches 16; Conserv
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; ORGANISM: Homo
US-09-866-108A-4013
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16;
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Matches
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GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: J, Yongquag

APPLICANT: J, Yongquag

APPLICANT: BENN, Sharron G.

APPLICANT: HENN, Sharron G.

APPLICANT: HANK, David R.

APPLICANT: RANK, David R.

APPLICANT: SHARNON, Mark

APPLICANT: SHARNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: ACOM.Co.-2.5

FILE REPERENCE: ACOM.Co.-0.-25

FRIOR PAPLICATION NUMBER: US 60/207,456

PRIOR PELING DATE: 2000-0.0-40

PRIOR APPLICATION NUMBER: GE 24263.6

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR PELING DATE: 2001-01-30

PRIOR PE
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                     TITLE OF INVENTION: Screening And Use Of Reagents Which Block Or Activate TITLE OF INVENTION: Intein Splicing Utilizing Natural Or Homologous Exteins FILE REFERENCE: PROTEIN SPLICING (FRAN/ERIC)
CURRENT APPLICATION NUMBER: US/09/430,221
CURRENT FILING DATE: 1999-10-29
EARLIER APPLICATION NUMBER: 08/811,492
EARLIER APPLICATION DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 3; Length 39; . 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.5%; Score 15; DB Best Local Similarity 78.3%; Pred. No. 1e+C Matches 18; Conservative 0; Mismatches
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Patent No. 6666188
SEQ ID NO 4012
LENGTH: 25
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US-09-866-108A-4012
Sequence 4012, Application US/09866108A
; Patent No. 6666188
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88.98;
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SEQ ID NO 27
LENGTH: 39
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US-09-866-108A-4012
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Best Local Similarity
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Gaps

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Indels

Length 25;

Gaps

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Length 25; 2; Indels

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PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 4015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14.8; DB 3;
Pred. No. 1.2e+03;
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88.9%;
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DATE: 2001-01-30
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HANZEL, David K.
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Best Local Similarity 88.9
Matches 16; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MARK
TITLE OP INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-0-24
PRIOR PILING DATE: 2000-0-0-4
PRIOR PILING DATE: 2000-0-0-4
PRIOR PILING DATE: 2000-0-0-27
PRIOR PILING DATE: 2000-0-0-27
PRIOR PILING DATE: 2001-01-30
             APPLICANT: SHANNON, MARK

1TILLE OF INVENTION: MAYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILLE REPERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30
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Pred. No. 1.2e+03;
0; Mismatches 2; Indels
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88.9%;
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HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.9
Matches 16; Conservative
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APPLICANT: GU, Yizhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-09-866-108A-4015
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APPLICANT:
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APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MAYK
APPLICANT: SHANNON, MAYK
APPLICANT: SHANNON, MAYK
TITUB OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/203.6
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PLILING DATE: 2001-01-30
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SOFTWARE: Abonica Sequence Listing Engine
PRED NO 4016
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Sequence 4016, Application US/09866108A
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: H, Yonggang
APPLICANT: H, Yonggang
APPLICANT: H, Yonggang
APPLICANT: HANK, David K.
APPLICANT: HANK, David K.
APPLICANT: ARANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
ITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AROMCA-7
CURRENT SHINNON, MARE: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
FRIOR APPLICATION NUMBER: US 60/236,359
FRIOR APPLICATION NUMBER: US 60/236,359
FRIOR PRICE TILING DATE: 2000-09-27
FRIOR APPLICATION NUMBER: US 60/236,359
FRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
                                  APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
                                                                                                                   CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2001-05-25

FRIOR PAPLICATION NUMBER: US 60/207,456

FRIOR PAPLICATION NUMBER: US 60/207,456

FRIOR PAPLICATION NUMBER: US 60/207,456

FRIOR PAPLICATION NUMBER: US 60/236,359

FRIOR APPLICATION NUMBER: GB 24263.6

FRIOR APPLICATION NUMBER: CT/US01/00666

FRIOR PILING DATE: 2000-09-27

FRIOR PAPLICATION NUMBER: PCT/US01/00667

FRIOR APPLICATION NUMBER: PCT/US01/00667

FRIOR APPLICATION NUMBER: PCT/US01/00669

FRIOR APPLICATION NUMBER: PCT/US01/00669

FRIOR PILING DATE: 2001-01-30

FRIOR PELING DATE: 2001-01-30

FRIOR APPLICATION NUMBER: PCT/US01/00668

FRIOR PILING DATE: 2001-01-30

FRIOR PILING DATE: 2001-01-30
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Pred. No. 1.2e+03;
0; Mismatches 2;
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Patent No. 6686188
SEQ ID NO 4018
LENGTH: 25
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88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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APPLICANT: GU, Yizhong

APPLICANT: GU, Yonggang

APPLICANT: HANZEL, David K.

APPLICANT: RANK, David R.

APPLICANT: RANK, David R.

APPLICANT: RANK, David R.

APPLICANT: RANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE OF INVENTION: MYOSIN-LIKE GENE COURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT APPLICATION NUMBER: US/09/866,108A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-04
PRIOR PELICATION NUMBER: US 60/236, 359
PRIOR PELICATION NUMBER: US 60/236, 359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
                                      Gaps
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61.7%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels
                                      Indels
   Pred. No. 1.2e+03;
0; Mismatches 2;
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Patent No. 6686188
SEQ 1D NO 4017
LENGTH: 25
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Patent No. 6666188
GENERAL INFORMATION:
APPLICANT: GI, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PRIN, Sharron G.
APPLICANT: RANK, David K.
APPLICANT: RANK, David K.
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88.98;
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                                      16; Conservative
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US-09-866-108A-4017
Best Local Similarity
Matches 16; Conserva
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US-09-866-108A-4017
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Gaps

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APPLICANT: Escobedo, Jaime.

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor CURRENT APPLICATION NUMBER: US/09/371,772B

CURRENT FILING DATE: 1999-08-10

PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR PILING DATE: 1995-10-26

PRIOR APPLICATION NUMBER: US 88/584,040

PRIOR FILING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 14225

SOFTWARE: Patentin version 3.0

SEQ ID NO 12797

LENGTH: 36
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; Sequence 12964, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
    APPLICANT: Ribozyme Pharmaceuticals, Inc.
    APPLICANT: Pavco, Pam
    APPLICANT: Baccobed, Jam
    APPLICANT: Escobedo, Jaime
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditi;
    TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditi;
    TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditi;
    TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditi;
    TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditi;
    TITLE NO FINVENTION: Method and Reagent for the Treatment of Diseases or Conditi;
    FILE REFERENCE: MBHBOO, 876-J (227/198)
    CURRENT FILING DATE: 1999-08-10
    PRIOR FILING DATE: 1999-08-10
    PRIOR FILING DATE: 1996-01-08
    NUMBER OF SEQ ID NOS: 14225
    SOFTWARE: PatentIn version 3.0
    SEQ ID NO 12964
    LENGTH: 36
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; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12964
                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
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Pred. No. 1.3e+03;
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US-09-371-772B-13173
; Sequence 13173, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Matches 14; Conservative
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US-09-371-772B-12964
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APPLICANT: Stinchcomb, Dan
APPLICANT: Bacobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE REPERENCE: MBHBRO, 387-70 (237/198)
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR TILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
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Pred. No. 1.3e+03;
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Patent No. 6886188
SEQ ID NO 4019
LENGTH: 25
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
          PCT/US01/00669
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; Sequence 12719, Application US/09371772B
; Patent No. 6566127
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Best Local Similarity 88.9%;
Matches 16; Conservative C
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Best Local Similarity 77.8%;
Matches 14; Conservative
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
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US-09-371-772B-12797
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LENGTH: 36
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pequence 14110, Application US/US/1/12B
petent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: RavCo. Pau
APPLICANT: BavCo. Pau
APPLICANT: BravCo. Pau
APPLICANT: Stinchcomb, Dan
APPLICANT: Marbod and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-10-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14110
LENGTH: 36
  Sequence 14110, Application US/09371772B
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77.8%;
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Best Local Similarity 77.8<sup>1</sup>
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: RNA
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Revo. Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stobedo, Jaime
TITLE OF INVENTION: McVels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-01-026
PRIOR FILING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 14225
SEQ ID NO 14087
LENGTH: 36
                                    APPLICANT: MCSWiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00, 976-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
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US-09-371-772B-14087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
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61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.38+03;
Matches 14; Conservative 2; Mismatches 2: Indela
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                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/005, 974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SSOFWARE: Patentin version 3.0
LENGTH: 36
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-09-371-772B-14087
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                              APPLICANT:
APPLICANT:
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; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-14110
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                                                                                                                                                                                    Length 36;
                                                                                                                                                                         Query Match 61.7%; Score 14.8; DB 3; Length 3 Best Local Similarity 77.8%; Pred. No. 1.3e+03; Matches 14; Conservative 2; Mismatches 2; Indels
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Pred. No. 1.3e+03;
2; Mismatches 2;
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RESULT 24 US-09-371-772B-14110

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-479-005A-938
             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT'R RIDOSYME PHARMACCULICALS, INC.
TILE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFERENCE: MBHB00-884-C
CURRENT APPLICATION NUMBER: US/09/479,005A
CURRENT APPLICATION NUMBER: US 09/444,209
PRIOR APPLICATION NUMBER: US 09/159,274
PRIOR FILING DATE: 1998-01-19
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 1208
SOFTWARE: Patentin Version 3.0
SEQ ID NO 938
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;Patent No. 5519127
APPLICATT: SHAH, JYOTSNA;BUHARIN, AMELIA;LANE, DAVID J.
TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
;PNEUMOCYSTIS CANTINII
;UWHBER OF SEQUENCES: 57
;CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 36;
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1S-09-36-196G-42756/A

1S-09-316-196G-42756/A

1Sequence 42756, Application US/09396196G

1Patent No. 6821724

1GENERAL INPORMATION:

1 APPLICANT: Michael Mittmann

2 APPLICANT: Michael Mittmann

3 APLICANT: Michael Mittmann

3 APLICANT: Michael Mittmann

4 APLICANT: Michael Mittmann

5 APPLICANT: Michael Mittmann

7 ITLE OF INVENTION: Methods of Genetic Analysis

7 ITLE OF INVENTION: MUMBER: US/09/396,196G

1 CURRENT APPLICATION NUMBER: 60/100,678

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR PILING DATE: 1999-09-17

1 NUMBER OF SEQ ID NOS: 127806

1 SOFTWARE: FastSEQ for Windows Version 4.0

1 SEQ ID NO 42756
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Pred. No. 1.3e+03;
2; Mismatches 2;
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Application US/09479005A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Best Local Similarity 75.0
Matches 18; Conservative
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US-09-479-005A-785
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; Sequence 785, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFREENCE: MBHB00-884-C
; CURRENT APPLICATION NUMBER: US 09/479,005A
; CURRENT FILING DATE: 1990-11-19
; PRIOR FILING DATE: 1998-09-22
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PATENTI VERSION 3.0
                                                             Sequence 665, Application US/09479005A

Sequence 665, Application US/09479005A

Patent No. 6656731

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity

FILE REPRENCE: MBHB00-884-C

CURRENT APPLICATION NUMBER: US/09/479,005A

CURRENT FILING DATE: 1999-11-19

PRIOR APPLICATION NUMBER: US 09/159,274

PRIOR FILING DATE: 1998-09-22

PRIOR FILING DATE: 1998-09-22

PRIOR FILING DATE: 1999-09-22

NUMBER OF SEQ ID NOS: 1208

SOFTAME: PatentIn version 3.0

LENGTHARE: PatentIn version 3.0
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US-09-479-005A-938
                                    SULT 26
-09-479-005A-665
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US-09-479-005A-785
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Batent No. 6566127

GENERAL INFORMATION:
APPLICANT: Ribosyme Pharmaceuticals, Inc.
APPLICANT: Rocasingen, Jim
APPLICANT: Bacobedo, Jane
APPLICANT: Escobedo, Jane
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refire Reference: Method and Reagent for the Treatment of Diseases or Conditions Refire Reference: Method and Reagent for the Treatment of Diseases or Conditions Refire Reference: Method and Reagent for the Treatment of Diseases or Conditions Refire Reference: Method and Reagent for the Treatment of Diseases or Conditions Refire Reference: Method and Reagent for the Treatment of Diseases or Conditions Refire Reference: Method and Reagent for the Treatment of Diseases or Conditions Refire Reference: Method and Reagent for the Treatment of Diseases or Conditions Refire Reference: Method and Reagent for the Treatment of Diseases or Conditions Refire Reference: Method and Reagent for the Treatment of Diseases or Conditions Refired Reference: Method and Reagent for the Treatment of Diseases or Conditions Refired Reference: Method and Reagent for the Treatment of Diseases or Conditions Refired Reference: Method and Reagent for the Treatment of Diseases or Conditions Refired Reference: Method and Reagent for the Treatment of Diseases or Conditions Refired Reference: Method and Reagent for the Treatment of Diseases or Conditions Refired Reference: Method 
                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid US-09-371-772B-12727
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US-09-371-772B-12754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.2; DB 3;
Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
PRIOR APPLICATION NUMBER: US 08/584,040 PRIOR FILING DATE: 1996-01-08 NUMBER OF SEQ ID NOS: 14225 SOFTWARE: Patentin version 3.0 SEQ ID NO 12727 LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GAAGUGAUGGCAUGCACUA 20
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Best Local Similarity 73.7%;
Matches 14; Conservative
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ORGANISM: Artificial Seguence
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Best Local Similarity 73.7<sup>3</sup>
Matches 14, Conservative
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US-09-371-772B-12754
DS-09-371-772B-12754
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APPLICANT: Maskingen, Jim
APPLICANT: Maskingen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MHHB00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US 60/9371,772B
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR PRIOR PAPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SEQ ID NO 12724
LENGTH: 36
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APPLICANT: Standboomb, Dan
APPLICANT: Batnehoomb, Dan
APPLICANT: Batnehoomb, Dan
APPLICANT: Batnehoomb, Dan
APPLICANT: Bacobedo, Jaine
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/09/371,772B
PRIOR TPLING DATE: 1999-08-10
PRIOR PILING DATE: 1999-10-26
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US-09-371-772B-12724
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Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
        US/07/826,657
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APPLICATION NUMBER: US/07/8
FILING DATE: 21-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 392,679
FILING DATE: 11-AUG-1989
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Best Local Similarity 73.7%;
Matches 14; Conservative
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Matches 18; Conservative
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US-09-371-772B-12724
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APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Secobedo, Jaime
APPLICANTON Method and Reagent for the Treatment of Diseases or Conditions .
TITLE OF INVENTION: Method and Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR PLING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12890
LENGTH: 36
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US-09-371-772B-12861
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Levels of Vascular Endothelial Growth Factor Receptor
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Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 3;
                    FILE REFERENCE: MBHB00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-08
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-371-772B-12890
; Sequence 12890, Application US/09371772B
; Patent No. 6566127
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Matches 14; Conserva
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Sequence 12819, Application US/09371772B
Sequence 12819, Application US/09371772B
Sequence 12819, Application US/09371772B
SENERAL INFORMATION:
APPLICANT: Pavco, Pam
APPLICANT: Bacobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR FILING DATE: 1999-08-10
PRIOR FILING DATE: 1996-10-26
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn Version 3.0
SEQ ID NOS: 12819
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TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
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; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12767
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11 Similarity 73.7%; Pred. No. 2.4e+03;
14; Conservative 2; Mismatches 3;
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59.2%; Score 14.2; DB 3;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 3;
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Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
  CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR PTILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Artificial Sequence
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Matches 14; Conserva
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US-09-371-772B-12861
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LENGTH: 36
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APPLICANT: Stinchcomb, Dan
APPLICANT: Becobed, Jaime
TITLE OF INVENTION: Mechod and Reagent for the Treatment of Diseases or Conditions R
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
GURRENT APPLICATION NUMBER: US/09/371,72B
CURRENT FILING DATE: 1995-08-10
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NO 12978

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59.2%; Score 14.2; DB 3;

Best Local Similarity 73.7%; Pred. No. 2.4e+03;

Matches 14; Conservative 2; Mismatches 3;
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Ribozyme Pharmaceuticals, Inc.
Pavco, Pam
McSwiggen, Jim
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ORGANISM: Artificial Sequence
PEATURE:
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Sequence 12962, Application US/09371772B

Patent No. 656617

GENERAL INPORMATION:

APPLICANT: Ribozyne Pharmaceuticals, Inc.

APPLICANT: Rescobed, Jain

APPLICANT: Escobed, Jaine

APPLICANT: Escobed, Jaine

APPLICANT: MESCOPED, Jaine

APPLICANT: MESCOPED, Jaine

APPLICANT: MESCOPED, Jaine

APPLICANT: MESCOPED, Jaine

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBHB00, 976-10 (237/198)

CURRENT FILING DATE: 1999-08-10

PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR PILING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 14225

SEQ ID NO 12962

LENGTH: 36
                 APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REPERBLOCE: MBHBOG, 286-0, 237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NO 12939
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12939
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Matches 14; Conservative
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Run on:

Sequence:

Searched:

Database

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CC326423
XN495 BayGenomics Gene Trap Library pGT2Lxf Mus musculus cDNA, mRNA sequence.
CC326423.1 GI:30795594
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Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by S. RACE of total RNA from gene trap ES
sequence tag generated by S. RACE of total RNA from gene trap ES
cell line. BS cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
CELL_LINE&KEY=XN495
                                                                         AV947544 AV947544
BH663108 SALK 0931
BH863117 SALK 0931
BH863151 SALK 0932
AQ902826 K071087-T
CC039454 3591 1.10
BH891758 3526_1_19
AAG00111 AAAB1GOPS
CRO86418 REVERSE S
CZ473756 G04146-39
AZ281223 ZM0093G24
AZ386728 1M0145620
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AZ386730 BMS MUSCU
AK109013 MUS MUSCU
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AJ669015 AJ669015
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
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BayGenomics.
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/clone_lib="BayGenomics Gene Trap Library pGT2Lxf"
/note="Vector: pGT2Lxf"
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/organism="Mus musculus"
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BH863151
AQ902826
CC039454
BH891758
AAG00111
CR066418
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AZ386728
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Unpublished (2001)
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DEFINITION
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AUTHORS
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JOURNAL
COMMENT
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AW100845 add2b05.r
AJ795163 AJ795163
CP331176 NACL--07-
AV835593 AW839593
AZI019594 ua91a06.r
CT017058 KBFH128N1
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AZ840176 2M0136B09
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BF347447 602020763
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BJ032969 BJ032969
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                                                                                                                                               December 13, 2005, 12:51:49; Search time 2984 Seconds (without alignments) 376.304 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                      41078325 seqs, 23393541228 residues
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AZ776950
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DR49P1S
                                                                                                            nucleic search, using sw model
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AU104991
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CF331176
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 su
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9b htc:*
9b est4:*
9b est6:*
9b est7:*
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Match Length DB
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gb_est2:*
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Gaps

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Result

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/clone_lib="Gm-c1008"
/clone_lib="Gm-c1008"
/note="Vector: pSPORT1; Site_l: SalI; Site_2: NotI; This coll a library was constructed from mRNA isolated from whole young pods, approximately 2cm long, of 12-week-old greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a NotI restriction site. SalI linkers adapters were ligated to the bluut-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-salI restriction site of the pSPORTI vector. The ligated cDNA fragments were transformed into E. coli Electrowax DHJOB host cells. This library was constructed
                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. Putative full
length read vector to vector length is 50 This clone is available
through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA
(phone: 800 423 4163; email: info@biogeneticservices.com)
Insert Length: 2346 Std Error: 0.00
Seq primer: -40RP from Gloco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ795163 Antirrhinum majus whole plant Antirrhinum majus cDNA clone AJ795163 Antirrhinum sequence.
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Wkaryota, Viridplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiids, Lamiales, Plantaginaceae, Antirrhineae,
   Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
Saedler,H. and Zachgo,S.
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
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                                                                                                                            Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1008-874"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by Dr. Lila Vodkin and Dr. Anu Khanna."
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/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antirrhinum majus (snapdragon)
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Best Local Simi
Matches 16;
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AJ795163/c
LOCUS
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                                                                   TITLE
JOURNAL
COMMENT
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KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
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                                                                                                                                                            CV933697 31 bp mRNA linear EST 25-JAN-2005 PMTpcm_3637 mating of 88069 (A1) and 618 (A2) Phytophthora infestans cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I (Gases I to 31)
Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
Mulndass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
Lam,S.T. and Judelson, H.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The form of the state of the st
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Large-scale gene discovery in the oomycete Phytophthora infestans reveals likely components of phytopathogenicity shared with true
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, stramenopiles, Oomycetes, Pythiales, Pythiaceae,
Phytophthora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Phytophthora infestans"
/mol_type="mkNa"
/mol_type="mkNa"
/db_xref="taxon:4787"
/eox="Al and A2"
/cone lib="mating of 88069 (A1) and 618 (A2)"
/note="Vector: pSPORT1"
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80.0%; Pred. No. 1.5e+05;
tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOI_ Plant-Microbe Interact. 18 (3), 229-243 (2005)
15782637
                                                                                                                                                                                                                                                                                                                                                                          Phytophthora infestans (potato late blight agent)
Phytophthora infestans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Plant Pathology
University of California
Webber Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: howard.judelson@ucr.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAGCGGAGTGATGGCAAGCA 20
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                                                                                                                                                                                                                                                                   CV933697
CV933697.1 GI:58123312
28 CCGAGTGATGCCCAGCAGGA
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nes 16; Conservative
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LOCUS
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PUBMED

COMMENT

FEATURES

ORIGIN

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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bumania; Butheria; Buarchontoglires; Glires; Rodentia;

Sciutognathi; Murcidea; Muridae; Murinae; Mus.

1 (bases 1 to 46)

Marra M. Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI019594

ua91a06.rl Soares mammary gland NDMMG Mus musculus cDNA clone
IMAGE:1364818 5' Fimilar to SW:HBP HUMAN Q00341 HIGH DENSITY
LIPOPROTEIN BINDING PROTEIN ;, mRNA sequence.
                                                                                   AVB39593 Nori Satoh unpublished cDNA library, young adult Ciona intestinalis cDNA clone rciad06f24, mRNA sequence.
                                                                                                                                                                                                                              Ciona intestinalis
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 40)
Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young
adult"
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Salyo-ku, Kyoto, Kyoto 606-8502, Japan
Fel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.2%; Score 13; DB 1; I 66.7%; Pred. No. 2.9e+05; tive 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Ciona intestinalis"
|mol Lype="mkNA"
|db xref="texon:719"
|clone="rciad06f24"
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/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL-07-D03"
/tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_l: BcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bhrhartoideae; Oryzeae; Oryza.

Enthartoideae; Oryzeae; Oryza.

Enthartoideae; Oryzeae; Oryza.

Exim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                         Query Match
55.8%; Score 13.4; DB 1; Length 42;
Best Local Similarity 73.9%; Pred. No. 1.9e+05;
Matches 17; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                       /organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:151"
/clone="018 3 07 e21"
/tissue type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhaham@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                 Molekulare Pflanzengenetik
MPI fuer Zuechtungsforsechung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
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                            Contact: Schwarz-Sommer Z
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Best Local Similarity
Matches 15; Conserv
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

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REFERENCE AUTHORS

RESULT 5 CF331176/c DEFINITION

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Gaps

us-10-713-137-2.sizlim.rst

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/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrH128N12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="UUGC2M0011H04"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                             17; Conservative
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Class: BAC ends
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Matches 17
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AUTHORS
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AZ776950
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                                                                                                                                                                                                                                                                                                    KBrH128N12 genomic clone, KBrH (HindIII) BAC library Brassica rapa eubsp. pekinensis, genomic survey sequence.
CT017058.1 GI:71469781
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beleffeld, Germany
Contact: Bernd Weisshaar
Contact: Bernd Weisshaar
Beleffeld University, Institute for Genome Research
Universitatesetrase 25, D-33594 Bielefeld, Germany Email:
bernd.weisshaar@uni-bielefeld.de
BAC end sequences of Brassica rapa BAC clone KBH128N12; generated
as contribution to the 'Multinational Brassica rapa Sequencing
Project' Seq primer: m13f TGTAAAAGGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (Dases I to 28)
Li,Y. and Weisshaar,B.
Direct Submission
Submitted (09-AUG-2005) Weisshaar B., Bielefeld University,
Institute for Genome Research, Universitaetsstrasse 25, D-33594
 Email: mouseest@watson.wustl.edu
Inis clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:898038
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                                                                                 Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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BAC end sequences of Brassica rapa
Unpublished
                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:1364818"
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                                                                                                                                                                                                                                                                                          'sex-"male"
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Best Local Similarity 76.23
Matches 16; Conservative
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2M0011H04F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0011H04 F, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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/clone_lib="Mouse 10kb plasmid UUGCNI library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Waiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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                                                                                                                                                                                                                                /clone_lib="KBrH, Brassica rapa HindIII BAC library GF-SCF-1002, Vector: pCUGIBac1" /lab_host="E.coli DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                Length 28;
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/strain="chiftu type 401-42"
/cultivar="Chiffu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                53.3%; Score 12.8; DB 11; 70.8%; Pred. No. 3.5e+05;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: H column: 04
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymersae and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoreasis. Vector DNA was prepared from a derivative of pwm92 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIL0-Gold (Stratagene) cells and selected for ampicillin resistance."
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AU104990
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Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail contact:
humquery@sanger.ac.uk Unpublished
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1 (bases 1 to 49)
Humphray, S. J., Huckle, E. and Hunt, S. B.
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  was hydrodynamically sheared by repeated passage through
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Danio rerio genomic clone DKEY-49P1, genomic survey sequence.
AL981974
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
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Pred. No. 3.7e+05;
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/db_xref="taxon:7955"
/clone="DKEY-491"
/tissue_type="Testis"
/note="vector pindigoBAC-536"
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53.3%; Score 12.8; DE
Best Local Similarity 87.5%; Pred. No. 3.764
Matches 14; Conservative 0; Mismatches
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymcrase and T4 day to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM22 (gi|4732114|gb|RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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AZ840176
AZ840176.1 GI:13010084
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia;
Sciurognathi, Muridea, Muridae, Murinae; Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,
Moderhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
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Insert Length: 10000 Std Error: 0
Plate: 0136 row. B column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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'strain="C57BL/6J"
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clone="UUGC2M0136B09"
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Location/Qualifiers
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Mus musculus
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Matches 14; Conservative
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Fax: 801 585 7177
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Best Local Similarity 87.5%,
Conservative
Take 14, Conservative
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CA913527/c
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Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzuki@ima.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Suzuki, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tckyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                  Hominidae, Homo.

1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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1 (Dases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Suyama, A. and Sugano, S. Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dclone="HRC07124"
/clone_lib="Sugano Homo sapiens cDNA library"
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   NU104990.1 GI:13554511
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                                                               sapiens (human)
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Best Local Similarity 87.5'
Matches 14; Conservative
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PCS01597X5 Scarlet Runner Bean Suspensor Region TriplEx2 Phaseolus coccineus CDNA 5' similar to sal85c10.y1 Gm-c1063 Glycine max cDNA, mRNA sequence.
CA913527.1 GI:27400519
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugamo,S. Construction and characterization of a full
1-length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 50)

Suzuki,Y., Taira.H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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                                                                       /clone_"HRC09325"
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Pred. No. 3.7e+05;
0; Mismatches 2;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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SM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muscidae; Muscida
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ZM009BH06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M009BH06 F, genomic survey sequence.
                                                                                                                                                     Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Barity Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo.Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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/db_xref="twon:9606"
/db_xref="zxV6C413"
/clone_lib="Sugano Homo sapiens cDNA library"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: Plate: 0098 row: H column: 06
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC2M0098H06"
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Location/Qualifiers
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Best Local Similarity
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/note="Organ: Suspensor Region of Globular-Stage Embryos;
/vector: TriplEx2; Site !: Sfilth; Site 2: Sfilth; Suspensor regions were micro-dissected from globular-stage embryos six days after pollination from greenhouse-grown plants [Weterings et al., Plant Cell 13, 2409-2425 [2001].
// Double-stranded CDNA was synthesized from suspensor mRNA using the SMART cDNA Library Construction Kit according to the manutacturer (Clontech). The suspensor cDNA fragments were directionally ligated into the Sfil restriction site of the lambda TriplEx2 vector (Clontech), and the recombinant cDNAs were transformed into E. coli XLI-Blue cells (Clontech). Suspensor CDNA plasmids used of directional sequencing were obtained by in vivo excision from the lambda TriplEx2 recombinants in E. coli BM25.8
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                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosida; eurosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phageolus.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Molecular, Cell, & Developmental Biology
University of Malfornia, Los Angeles
621 Charles E. Yaung Drive South, Los Angeles, CA 90095-1606, USA
Tel: 310 825 3270
Fax: 310 825 8201
                                                                                                                                                                                                                                             1 (bases 1 to 42)
Bui,A.Q., Le,B.H., Weterings,K., Bi,Y.-P., Choi,J.-S.,
McBlroy,K.E., Choi,P.S., Harada,J.J., Fischer,R.L. and
Goldberg,R.B.
Gene Activity in Different Regions of a Post-Fertilization Plant
Bmbryo by EST Analysis
Unpublished (2002)
Contact: Goldberg, R.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Organism="Phaseolus coccineus"
|mol type="mRNA"
|cultivar="Hammond's Dwarf Scarlet"
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Pred. No. 4.5e+05;
0; Mismatches 4;
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AU108033
AU108033.1 GI:13557555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: bobg@ucla.edu
Seg primer: 5' TriplEx
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78.9%;
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                                                             Phaseolus coccineus
Phaseolus coccineus
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nes 15; Conserv
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Location/Qualifiers
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                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gb]AR125072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sa30a08.x1 Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1004-783 3' similar to TR:Q39827 Q39827 ARGININE DECARBOXYLASE.
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Shoemaker, R. Kethin, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoemaker, R., Kethin, P., Wodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Undarra, M., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCani, R., Waterston, R. and Wilson, R., Jackson, Y., Cardenas, M.,
Public Soybean EST Project
Unpublished (1999)
Public Soybean EST Project
Public Soybean EST Project
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When it has been determined, an EST from the other end of this
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTS on clone' field. Trace
considered overall poor quality Possible reversed clone: similarity
on wrong strand This clone is available through: Biogenetic
Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423
Services, 801 primer: -400P from Gibco
High quality sequence stop: 1
POLYA=No.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse l0kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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/clone lib="Gm-clood"
//note="Wector: pBluescript II XR; Site_I: ECORI; Site_2:
Xhoi; Root cDNA. The mRNA was isolated from entire roots
of 8 day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's cDNA
Synthesis Kit (catalog #200401) was used to synthesize the
cDNA. First- strand synthesis was performed with 5-methyl
dCTP, hence the ligated cDNA is heminethylated.
Stratagene's first-strand synthesis primer was used
[GAGAGAGAGAGAGACACATGATCTCGGA(7)-18] After
second-strand synthesis, the cDNA ends were 'polished'
with clone Febr DNA polymerase, 'ligated to EcoRI adapters,
and phosphorylated The XDNA could be protected by their
heminethylated status. The cDNA would be protected by their
heminethylated status. The CDNA constructs were
size-fractionated with a 500bp cutoff, using Gibcobr. Life
Technologies' cDNA Size Fractionation column. The column
eluent was then ligated into Stratagene's pBluescript II
XR Predigested vector (pBluescript II SK(+) that had been
digested victo (pBluescript II SK(+) that had been
sequenced, and plossess putative cDNA inserts. This library
was constructed by Dr. Paul Keim & Virginia H Coryell,
Department of Biology, Box5640, Northern Arizona
University, Flagsteff, AZ 86011, Phone: 520-523-1078 (Pr.
Paul Keim), $20-523-1372 (Virginia H. Coryell),
Paul Keim), $20-523-1372 (Virginia H. Coryell),
Fax:
$20-523-7500, email: paul.keim@nau.edu,
virginia.coryell@nau.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF347447 37 bp mRNA linear EST 22-NOV-2000
6020020355F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156238
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 37)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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                                                                                                               'db_xref="taxon:3847"
'clone="GENOME SYSTEMS CLONE ID: Gm-c1004-783"
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organism="Glycine max"
                                                                                                                                                                                                      /tissue_type="root"
/lab_host="XL10-Gold"
                                         /mol_type="mRNA"
/cultivar="Williams"
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units. For more information on RescueMu, go to the wet site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BgHII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressed genes in X. laevis embryo
Expressed (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Ill Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                       51.7%; Score 12.4; DB 9;
llarity 72.7%; Pred. No. 5.6e+05;
Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Xenopus laevis"
                                                                                                                                                                                                  plates with ampicillin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL019f12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: tshini@genes.nig.ac.jp
The information of this clone
URL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://xenopus.nibb.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 GCGGAGGCACGGAAGAAGAACAAC 1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 16; Conserv
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DEFINITION
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BJ032969/c
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CZ472229
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COMMENT
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Malbot V
Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH620252 10-JAN-2002 1007 - RescueMu Grid H Zea mays genomic, genomic survey sequence. BH620252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="1007 - RescueMu Grid H"
/clone lib="1007 - RescueMu Grid H"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007061 column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Brn67"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                   /mol_resurversions | molecular | molecular
                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9428 row: n column: 15 High quality sequence stop: 37. Location/Qualifiers
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/mol type="genomic DNA"
/culTivar="mixed background W23/A188/B73"
/db xref="texon:4577"
/tissue type="leaf"
/dev stage="adult"
/lab_host="BH10B"
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Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .44
/organism="Zea mays"
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nes 16; Conserv
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AUTHORS
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Matches
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32 bp mRNA linear EST 26-SEP-2003 laevis CDNA closer EST 26-SEP-2003 laevis cDNA close XL019f12 5', mRNA sequence. BJ032969.1 GI:17391810 EST.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CZ472229
33 bp DNA linear GSS 29-APR-20 d01430-3prime Exelixis P element XP insertions Drosophila melanogaster genomic Sequence recovered from 3' end of P element, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is available through the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="whole embryo"
/dev_stage="stage 15"
/clone_lib="NIBB Mochii normalized Xenopus neurula
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 32)
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
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0
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44;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poolideae; Triticeae; Hordeum.
1 (bases 1 to 38)
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1M0584P01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0584P01 R, genomic survey sequence.
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Mus musculus
Budsaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Budsaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Murcidea; Murinae; Mus.
1 (bases 1 to 38)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacrer, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Musse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="ghoots"
/dev_stage="germination"
/clone_lib="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare shoots germination"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                          Barley EST sequencing project in NIG and Okayama Univ Unpublished (2001)
Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazasto@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp,
Sato, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct submission;
                                                                                                                                                                                                                                                                                                                                                 database:http://www.shigen.nig.ac.jp/barley/Barley.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 38;
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|organism="Hordeum vulgare subsp. vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sub_species="vulgare"
/db_xref="taxon:112509"
/clone="bags11124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert Length: 10000 Std Error: (Plate: 0894 row: P column: 01 Seq primer: CACACAGGAAACAGCTATGACC class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="Haruna Nijo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                           Hordeum vulgare subsp. vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ773196.1 GI:12897306
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Best Local Similarity
Matches 14; Conserv
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                       ORGANISM
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AZ773196/c
                                                                                                                         AUTHORS
TITLE
                                                                                                                                                             JOURNAL
                                                                                                      REFERENCE
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                                                                         (SM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

Shibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A., Singh,C.M., Buchholz,R., Demsky,M. Fawcett,R., Francis-Lang,H.L., Greer,K., Marcuni,S.R., Howia,B., Erickson,C., Fisher,W.W., Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C., Soprozynski,C., Duyk,G., Winberg,M.L. and Margolis,J. A complementary transposon tool kit for Drosophila melanogaster
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Class: transposon insertion site.
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                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4018
Fax: 510 486 6798
Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of 1
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                                                          Drosophila melanogaster (fruit fly)
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CZ472229
CZ472229.1 GI:62966242
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Matches 14; Conservative
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Subsection of the search of th
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/strain="isogenic w- strain"
/db type="genomic Wastrain"
/db type="genomic w- strain"
/db type="genomic w- strain"
/db type="genomic w- strain"
/clone lib="Exelizis P element XP insertions"
/clone lib="Exelizis P element XP (GenBank accession number AY515149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsinscy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposaes, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                         The P element insertion position is 31 in the 38 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
                                              Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
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/db_xref="taxon:9823"
/clone="C0000048_C19"
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
Email: RHoskins@lbl.gov
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Sus scrofa
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Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;

Nooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilade; Drosophila.

I (bases 1 to 38)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resources (documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared but a constant velocity. The sheared but on oil inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone_lib="Mouse_10kb plasmid UUGCIM library." /note="Vector: PWD42nv; Purified genomic_DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
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                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0584P01"
         High quality sequence stop: 38 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
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GSS 05-AUG-2002
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/clone="SALK 093178"
/clone="SALK 093178"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Joske,A., Karnes,M., Kim,C.J., Parker,H., Frednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
Shinn,P., Zimmerman,J. and Ecker,J.R.
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A Sequence-Indexed Library of Insertion Mutations in the
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                                                                                                                                                                                                                                                                                                         This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At2g10530. Class: TDNA tagged. Location/Qualifiers
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 453 4100 x1752
                                                                                          Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Email: ecker@salk.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
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Unpublished (2001)
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Arabidopsis thaliana
Busaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
1 (bases 1 to 42)
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I (basea I to 47)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Contact: Nori Satoh
Department of Zoology
    /clone_lib="CSEQRANO9"
/note="Vector: pBlueScriptII(KS+); Site_l: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."
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/clome_lib="Nor1 Satch unpublished cDNA library, young
adult"-
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                                                                                                                                                  Length 44;
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                                                                                                                                                50.8%; Score 12.2; DB 1;
82.4%; Pred. No. 6.9e+05;
tive 0; Mismatches 3;
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Location/Qualifiers
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="whole animal"
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/db_xref="taxon:7719"
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AQ902826
K071087-T7 Library RPCI1,3-5 Human PAC Homo sapiens genomic clone RPCIP704K071087, genomic survey sequence.
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TDNA insertion lines Arabidopsis
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/clone="SALK 093883"
/clone="SALK 093883"
/clone="Ib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the aite of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Location/Qualifiers
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The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 453 4190 x1752
Fax: 858 6379
Email: ecker@salk.edu
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Larity 75.0%; Pred. No. 8.5e+05;
Conservative 0; Mismatches 5; Indels
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/mol_type="genomic DNA"
/ecotype="Col-0"
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                                             15 ggagrgarrtcaaaaacrac 34
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5 GGAGTGATGGCAAGCACGAC
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH863117 42 bp DNA linear GSS 05-AUG-2002 SALK 093195 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_093195, genomic survey sequence.
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/clone="SALK 093195"
/clone="SALK 093195"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R. A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)
                                                                                             /clone="SAIK 093187"
/clone lib="Ārabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At2g10530.
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                         50.0%; Score 12; DB 9; Length 42; 75.0%; Pred. No. 8.5e+05; ive 0; Mismatches 5; Indels
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  'organism="Arabidopsis thaliana"
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Arabidopsis thaliana
                          /mol_type="genomic DNA"
/ecotype="Col-0"
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/ecotype="Col-0"
                                                                        db xref="taxon:3702"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 GGAGTGATGGCAAGCACGAC 24
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pBlueScript backbone); Site 1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid P was grown at Molokai in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH108 cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp DNA linear GSS 14-AUG-2002
- RescueMu Grid K Zea mays genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Biological Sciences
Stanford University
Stanford University
Stanford University
Stanford University
Stanford University
Stania Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Benail: wabbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3526_1_1_1 row: 29
Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                           Score 12; DB 9; Length 47;
Pred. No. 8.6e+05;
0; Mismatches 5; Indels
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genomic survey sequence.
BH891758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:22222805
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Best Local Similarity 75...
Best Local 15; Conservative
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Walbot, V.
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BH891758.1
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                   E 1 (bases 1 to 44)

S Alexander,C., Bernstein,S.L., Rocchi,M. and Auburger,G.
Saturating Density of STS8 (1/6 kb) in a 1.1 Mb Region on 3q28-q29:
A Valuable Resource for Cloning of Disease Genes
L Unpublished (2000)
Contact: Alexander C
Department of Molecular Genetics
Institute of Ophthalmology, University College London
I1-43 Bath Street, London EC1V9EL, UK
Tel: +44 171 608 6833
Fax: +44 171 608 6833
Email: calexand@hgmp.mrc.ac.uk
Seq primer: 'nested' T7-Primer cggtcgagcttgacattgtag
Class: PAC end.
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Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 47)
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Unpublished (2001)
Unpublished (2001)
Unpublished (2001)
Stanford University
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Tel: 650 723 2227
Tel: 650 725 8227
Email: walbot/satanford.edu
Very probable ligation site of ends cut by single endonuclease.
Plate: 3591 1 104 1 row: 17
Class: transposon-tagged.
                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="RPCIP704K071087"
/clone lib="Library RPCI1,3-5 Human PAC"
/note="Human genomic PAC library RPCI (Ioannou et al.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Organism= deamidy DNA"
//mol_type="genomidy DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/db_tiseue type="lag"
/dev_stage="adult"
/dev_bost="mixed"
/dev_bost="mixed"
/dob_iost="mixed"
/dob_iost="mixed"
/dob_iost="mixed"
/dob_iost="mixed"
/dob_iost="mixed"
/dob_iost="mixed"
/dob_iost="lag'i Vector: RescueMu (engineered from /note="Organ: leaf;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 44;
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llarity 75.0%; Pred. No. 8.5e+05;
Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Zea mays"
/wol_type="genomic Dl
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Best Local Similarity
Matches 15; Conserva
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COMMENT
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KEYWORDS
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SM Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Brosophilidae; Drosophila.

I (bases 1 to 30)

I (bases 1 to 30)

I (bases 1 to 30)

Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,

Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,

Greer,K., Hartouni,S.R., Howie,B., Jakkula,L., Joo,D., Killpack,K.,

Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,

Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,

Swimmer,C., Kopczynski,C., Duyk,G., Winberg,M.L. and Margolis,J.

A complementary transposon tool kit for Drosophila melanogaster
                                                                                                                                                                                                                                               van der Weyden,L.,
Nishijima,I., Yu,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d04146-3prime Exelixis P element XP insertions Drosophila melanogaster genomic Sequence recovered from 3' end of P element, genomic survey sequence.

C2473756.1 G1:62967769
GSS.
                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Enarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Murinae, Musinae, Mus.

1 (bases 1 to 50)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Onokers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y. Rogers, J. and Bradley, A.

Direct Submission
Submitted (20-FBB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The P element insertion position is 1 in the 30 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
chromosome engineering clone MHPP182e10, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%; Score 12; DB 11; Length 50
75.0%; Pred. No. 8.7e+05;
ive 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPP182e10"
                                                                     GSS; genome survey sequence;
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="MHPP"
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                         CR086418
CR086418.1 GI:49820010
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Submitted (23-07-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue gaston Cremieux, 91057 Evry cedex, FRANCE
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutent line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program "Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr).
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                                                                                                                                                                                                                                                                 Arabidopsis thaliana T-DNA flanking sequence, right border, clone AJ600111
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T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                            Length 49;
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GSS; right border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="500C09"
                            Score 12; DB 9; I
Pred. No. 8.7e+05;
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          50.0%; Sco... 75.0%; Pred. No. co...
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EMBO Rep. 3 (12), 1152-1157 (2002)
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                                                                                                                           2 AGCGGAGTGATGGCAAGCAC 21
                                                                                                                                                                  26 AGCGGAGAGAGCTAGCCC 45
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Balzergue, S.
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Best Local Similarity 75.0
Matches 15; Conservative
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Matches 15: Congery
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CRO86418/c
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GSS 29-APR-2005

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gol electrophoresis. Vector DNA was prepared from a derivative of pMAD42 (gil 4732114)[gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xiii0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A2386728 Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0145C20R, genomic survey sequence.
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1 (bases 1 to 41)

Dunn, D., Aoyagi, Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longadre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
/clone_lib="Mouse_10kb_plasmid_UUGCIM_library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
84112, USA
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49.2%; Score 11.8; DB 9; Length 40;
Best Local Similarity 69.6%; Pred. No. 1e+06;
Matches 16; Conservative 0; Mismatches 7; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: C column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0145C20"
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                                                                                                                                                                                                  /u_xtell="cauchi:/zz/
/lone lib="Exelixis P element XP insertions"
/note="Vector: P element XP (GenBank accession number
/note="Vector: P element XP (GenBank accession number
AY515149); An isogenic w- Drosophia melanogaster strain
was mutagenized by remobilization of transposable
elements. For the P element XP, we selected an easily
mobilized ammunition element among inserts hopped onto the
Binsinscy balancer. New insertions were collected in vials
from dysgenic females using the standard chromosomal
source of transposase, delta2-3. All lines were mapped to
a chromosome by standard genetic methods, examined for
homozygous viability and used for recovery of flanking
genomic sequence by inverse PCR."
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1 (bases 1 to 40)

2 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Dasmid inserts

1 Unpublished (2000)

1 Unpublished (2000)

1 Contact: Robert B. Weiss

1 University of Utah Genome Center
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2M0093G24R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0093G24 R, genomic survey sequence.
AZ821223
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                                                                                                 /organism="Drosophila melanogaster"
|mol_type="genomic DNA"
| fetrain="1sogenic w- strain"
|db_xref="taxon:7227"
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Insert Length: 10000 Std Error: 0.00
Plate: 0093 row: G column: 24
Seg primer: CACACAGGAAACAGCTATGACC
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                       Class: transposon insertion site.
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/clone="UUGC2M0093G24"
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21 CACCGGAGTGAAGGC 7
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Fax: 801 585 7177
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Matches 16;
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                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymcrase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwDAQ2 (gql #4732114[gbl AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tm89g04.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2165334 3' similar to SW:WASP MOUSE P70315 WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG;, mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                           /clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
'lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
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                                                                                                                Laboratory Mouse DNA Resource
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/mol_type="mRNA"
/db_xref="taxon:9606"
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       /tissue type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/clone="IMAGE:2165334"
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	Adz75765 Human ind	Abk05395 Human NOG	Aah96727 Human Chk	Adv17621 Human PLN	Adu94766 Human TER	Abk05358 Human NOG	Adv47962 HBV G-cle	Adv04075 Human BAC	Adv04149 Human BAC	Adv04093 Human BAC	Adv17630 Human PLN	Adv04128 Human BAC	Abk59131 Human CLC	Acd53318 HBV G-cle	Adm61879 Hepatitis	Adc33588 Human loc	Aad00496 Clone cGM	Abk05366 Human NOG	Adv47946 HBV G-cle
	ID	ADZ75765	ABK05395	AAH96727	ADV17621	ADU94766	ABK05358	ADV47962	ADV04075	ADV04149	ADV04093	ADV17630	ADV04128	ABK59131	ACD53318	ADM61879	ADC33588	AAD00496	ABK05366	ADV47946
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Abk20721 Human ERG Acd53251 HBV G-cle Adm61863 Hepatitis Adm47991 Human ind Adu85578 Anti human TER Adu94721 Human TER Adu9468 Human TER Adu96363 Human TER Adu96363 Human TER Adu96364 Human CLC Adu86547 Human CLC Abk08475 Human CLC Abk08475 Human CLC Abk08475 Human CLC Abk08475 Human CLC Abk08496 Human TER Adu86540 Human TER Adu8640 Human TER Adu8640 Human CLC Abk0910 Human NOG Adv48009 HBV G-cle Adv48009 HBV G-cle Adu81331 HBV G-cle Adm61892 Hepatitis	ALIGNMENTS ynthase gene exon 7 forward PCR primer. ry edema; pulmonary edema; disease; SNP detection; allelic variation; inDIA. INDIA. gh altitude pulmonary edema (HAPE) by nducible nitric oxide synthase gene, and rences in the distribution of allelic glish.	Tell method for detecting predisposition to (HAPB). The method comprises amplifying e nitric oxide synthase (iNOS) gene mthesizing forward and reverse (765+ADZ75766), and predicting and							
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C of CD20 in the presence of a divalent cation that is preferably Mg^2/+.

C Furthermore, it may be contacted with a cell to reduce CD20 activity of the call and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more conformal and level and the level of CD20. The treatment may further comprise the use of one or more conformal lamphoma, leukaemia, B-cell lymphoma, low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, lymphocytic lumune thrombocytopaenia, and inflammatory arthropathy. The NOGO-treated with a cell to reduce NOGO est in the conformal conformal inflammatory arthropathy. The NOGO-treated with a cell to reduce NOGO estivity of the conformal cation that is preferably Mg^2/+. Furthermore, the coll and treat a patient having a condition associated with the level of conclet cand may be contacted with a cell to reduce NOGO activity of the conclet cand may further comprise the use of one or more therapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CNA, stroke), Altheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, and/or other neurodegenerative disease, musuallar dystrophy, and/or other neurodegenerative disease catatis which respond to the modulation of NOGO expression. The present sequence is a substrate sequence for a nucleic acid of the invention conclusion the human NOGO sequence for a nucleic acid of the present cated on the human NOGO sequence and a nu
                an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 78.3 tes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; checkpoint kinase-
RNA cleavage; cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-496922/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157206-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-OCT-2001
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AAH96727
            84966996999999999999999999999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; MOGO; hammerhead ribozyme; DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; I-ymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphome; NHL; lymphomy; leukaemia; MoL; immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntingcon's disease; substrate sequence; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
statistically analyzing differences in the distribution of the allelic variants in the populations, where GG genotype at 19480 position are at low risk of HAPE, and AA genotype at 19480 position are at the FAPE. The present sequence represents the forward oligonucleotide primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                         DB 14; Length 24;
                                                                                                                                                                                                                                                                                                                 100.0%; Score 24; DB 14; Length 2
100.0%; Pred. No. 0.18;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                            Sequence 24 BP; 7 A; 6 C; 9 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CAGCGGAGTGATGGCAAGCACGAC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAGCGGAGTGATGGCAAGCACGAC 24
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28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK05395 standard; RNA; 37
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(BLAT/) BLATT L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHOWRIRA B M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MCSWIGGEN J.
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                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                  the invention.
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                                    The present invention provides nucleic acid molecules capable of downregulating the expression of the human checkpoint kinase-1 (Chkl) gene. These may be antisense or ribozyme sequences, and are useful in the treatment of diseases associated with conditions affected by Chkl levels, including cancer. The present sequence is an oligonucleotide described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                          Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; hethera-2, human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; preseniln-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inoxyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; beast cancer; Alzheimer's disease; diabetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
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                                                                                                                                                 71.7%; Score 17.2; DB 4; Length 37; 77.3%; Pred. No. 3.1e+02; ive 2; Mismatches 3; Indels
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Matulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                           Sequence 37 BP; 11 A; 6 C; 13 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                    Human PLN G-cleaver ribozyme sequence #9
                                                                                                                                                                                                                  2 AGAGGAGUGAUGCACUA 23
                                                                                                                                                                                                     2 AGCGGAGTGATGGCAAGCACGA 23
              Claim 5; Page 68; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0151713P.
99US-0156236P.
99US-0156236P.
99US-0156467P.
99US-0169100P.
99US-0173612P.
99US-0173612P.
                                                                                                                                                                                                                                                                                            ADV17621 standard; RNA; 37 BP
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                                                                                                                                                               77.38;
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                                                                                                                                                                                                                                                                                                                                              10-FEB-2005 (first entry)
                                                                                                                                                               Best Local Similarity 77.3
Matches 17; Conservative
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Karpeisky A, N
Stinchcomb D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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04-FEB-2000;
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29-DEC-1999;
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                                                                                                                                                    Query Match
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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBR), protein kinase C alpha (PKC alpha), beta-secretaee (BACE), human epidermal growth factor receptor-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-claaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-claaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-claaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-claaver, amberzyme, and for treating cancer, in particular breast cancer, Alzheimer's disease, dispetes, obesity, cardiac diseases e.g. heart disease, as carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased calls and to detect the presence of specific RNA in a cell. The present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; Meth-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; e-erb; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; mepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; brancer; Alzheimer's disease; diabetes; obesity; cardiac disease; heart disease; agg-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 37 BP; 8 A; 6 C; 15 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human TERT G-cleaver ribozyme sequence #157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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                                                                                                     Example 5; Page 428; 717pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AGCGGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0151713P.
99US-00406643.
99US-0156236P.
99US-0156467P.
99US-00436430.
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                                                     obesity and heart disease.
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27-SEP-1999;
27-SEP-1999;
27-SEP-1999;
08-NOV-1999;
06-DEC-1999;
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ADU94766
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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (PKER2P-2), human telomerase (HTBRT), protein kinase C alpha (PKER2P-2P2), numan telomerase (HTBRT), protein kinase C receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presentlin-1 (ps-1), presentlin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucled nammerhead (HH), hairpin, NCH (inoxyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Althelmer's disease, diabetes, obesity, cardiac disease e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
                                                                                                                                                                                                                                                                                                                                                                   Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                          Chowrira B;
                                                                                                                                                                                                                                    Jøman N, Blatt L, Beigelman L, Burgin A;
Matulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16.8; DB 5; Length 36;
Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 36 BP; 8 A; 10 C; 12 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 304; 717pp; English.
                                                                                                                                                                                                                                 Blatt L,
                                                                                                                                                                                                                                 Usman N, Blatt L,
Matulic-Adamic J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.0%;
                                                                                20-MAR-2000; 2000US-00531025.
14-APR-2000; 2000US-0197769P.
23-MAY-2000; 2000US-0057823.
09-AUG-2000; 2000US-00638385.
                 99US-0173612P.
                                                            2000US-00498824
                                                                                                                                                                                         (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                              obesity and heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                         WPI; 2001-244406/25
                                                                                                                                                                                                                                                                              Stinchcomb D,
                                                                                                                                                                                                                                 Mcswiggen J,
Karpeisky A,
                                                            04-FEB-2000;
                 29-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human NOGO G-Cleaver substrate sequence #21.
                                                                                                                                                                                                                                                                                                   4 CGGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cecacione cecación de cecación
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK05358 standard; RNA; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
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The invention relates to a nucleic acid molecule which down regulates or gypeasion of a neurite growth inhibitor gene (NOGO). The nucleic acids (e.g. a ribozyme or a nucleic acids deaving an RNA molecule possessing an Inozyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NGW tripled), a zinzyme (cleaving RNA with a nucleic acid is used to cleave CC of CD20 in the presence of a divalent cartion that is preferably Mg^2+.

CC Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more core therapies. In particular, the CD20 targeting nucleic acid with the Nucleic acid is used to cleave RNA of the NOGO activity of the charman in mmunodeficiency virus) associated NHL, lymphoma, lumphoma (MCI), immunocytoma (IMC), small B-cell lymphoma (MCI), immunocytoma (IMC), small B-cell lymphomy. The NOGO corporated with the level of presence of a divalent cation that is preferably Mg^2+. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the contact a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-cragetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular a ccident (CNA, stroke), Alzheimer's disease, dementia, muscular disease, ataxia, Huntington's disease, cerebrovise disease, ataxia, Huntington's disease, cerebrook is aubstrate sequence for a nucleic acid of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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cerebrovascular accident, CVA, Alzheimer's disease, multiple sclerosis, chemctherspy-induced neuropathy, amyotrophic lateral sclerosis, ALS; Parkinson's disease, ataxia; Huntington's disease; substrate sequence; Creutzfeldt-Jakob disease; muscular dystrophy, neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a nucleic acid molecule which down regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37 BP; 5 A; 10 C; 17 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chowrira BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 89; Page 92; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence is a substrate sequence
based on the human NOGO sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     central nervous system injury.
                                                                                                                                                                                                                                                                                                                            11-FEB-2000; 2000US-0181797P.
28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
                                                                                                                                                                                                                                                                                 09-FEB-2001; 2001WO-US004273.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHOWRIRA B M
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Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               BLATT L.
                                                                                                                                                                                      WO200159103-A2.
                                                                                                                                                                                                                                                                                                                       11-FEB-2000;
                                                                                                                       sapiens
                                                                                                                                                                                                                                   16-AUG-2001
                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                           (RIBO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHOM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                               (BLAT/)
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                                                                                                                       Homo
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Gaps

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6e+02;

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Brzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; hetaPa-2, human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACB; human epidermal growth factor receptor-2; HER2; e-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; haltpin; NCH; innoxyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; bast cancer; Alzheimer's disease; diabetes; obesity; cardiac disease; heart disease; agg-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
diabetes, obesity, cardiac disease e.g. heart disease, age-related diseases, heptitis B infections, and heptitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a ribozyme used in the examples of the present invention. Note: Some SEQ 1D Nos are repeated more than once in the specification, but these have different sequences associated with them.
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Matulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                                                            Score 16.6; DB 5; Length 37;
Pred. No. 6e+02;
                                                                                                                                                                                                                    Sequence 37 BP; 8 A; 10 C; 12 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human BACE G-cleaver ribozyme sequence #12.
                                                                                                                                                                                                                                                                                                                                                  CAGCGGAGTGATGGCAAGCACGA 23
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99US-0156236P.
99US-0156467P.
99US-0169100P.
99US-0147432.
99US-0173612P.
99US-00476387.
2000US-00498824.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADV04075 standard; RNA; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                              Local Similarity 73.9 tes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-244406/25
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20-MAR-2000; 2
14-APR-2000; 2
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Karpeisky A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-1999;
27-SEP-1999;
08-NOV-1999;
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29-DEC-1999;
29-DEC-1999;
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                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                            Matches
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             22222222222
                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                              Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; hetherAP-2; human telomerase; hTERT; protein kinase Calpha; PKC alpha; beta-secretae; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; preseniln-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; innoxyme; G-cleaver; amberzyme; zinzyme; DNAxyme; cancer; baratises; disease; disease; disease; obesity; cardiac disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (FTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha, beta-secretase (BACE), human epidermal growth factor receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBN) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chowrira B;
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Matulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Page 531; 717pp; English.
                                                                                                                                                                                                                                                                                             HBV G-cleaver ribozyme sequence #57.
                 23
                                                      23
                                       CAGGGGGGGGGGCACUA
               CAGCGGAGTGATGGCAAGCACGA
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99US-00406643.
99US-0156236P.
99US-0156467P.
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99US-0169100P.
99US-00474432.
99US-0173612P.
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2000US-0197769P.
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                                                                                                                                                                  ADV47962 standard; RNA; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                obesity and heart disease.
                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus.
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Karpeisky A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2000;
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29-DEC-1999;
29-DEC-1999;
30-DEC-1999;
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08-NOV-1999;
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                                                                                                                                                                                                            ADV47962;
                                                                                                                          RESULT 7
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Chowrira

30-DEC-1999; 99US-00476387. 04-FEB-2000; 2000US-00498824. 20-MAR-2000; 2000US-0053102S. 14-APR-2000; 2000US-01977699. 23-MAY-2000; 2000US-00578223.

09-AUG-2000; 2000US-00636385

99US-0173612P

29-DEC-1999

us-10-713-137-2.sizlim.rng

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The present invention relates to the use of enzymatic nuclear actor also methods for their use to down regulate or inhibit the expression of also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyroaine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (MTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACB), human epidermal growth factor receptor-2 (FMEX/c-erb2/neu), phospholamban (PLN), presentlin-1 (ps-1), presentlin-2 (ps-2), and hepatitis by avivas (HBN) presentlin-1 (ps-1), presentlin-2 (ps-2), and hepatitis in the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, include hammerhead (HH), hairpin, MCH (inozyme), G-cleaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, and beraing cancer, in particular breast cancer, Alzheimer's disease, disease, obesity, cardiac diseases e.g. heart disease, age-related diseases, begatitis and hepaticis and hepatitis and hepaticis cald molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased calls and to detect the present cald molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased calls and to detect the present cald molecules can also be used as carcinoma. Note: Some SEQ ID Nos are repeated more than once in the sequence specification, but these have different sequences associated with them.
Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
                                                                                                                                                                                                                         The present invention relates to the use of enzymatic nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37 BP; 5 A; 9 C; 18 G; 0 T; 5 U; 0 Other;
                                                                                                                                                 Example 4; Page 364; 717pp; English.
                                                                        obesity and heart disease.
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Gaps .; 0 69.2%; Score 16.6; DB 5; Length 37; 73.9%; Pred. No. 6e+02; ive 2; Mismatches 4; Indels Best Local Similarity 73.9 Matches 17; Conservative Query Match

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1 CAGCGGAGTGATGGCAAGCACGA 23 1 ceccececencia de ceccencia de ceccecene de cecece de cecece de cecene d ò 셤

ADV04149 standard; RNA; 37 (first entry) 10-FEB-2005 ADV04149; RESULT 9 ADV04149

Human BACE G-cleaver ribozyme sequence #52.

Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; mepatitis B virus; HBV, hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberzyme; UNAzyme; DNAzyme; nancer; breast cancer; Alzheimer's disease; disabetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human:

Homo sapiens.

WO200116312-A2.

08-MAR-2001.

30-AUG-2000; 2000WO-US023998 31-AUG-1999; 27-SEP-1999; 27-SEP-1999;

990S-00406643 990S-0156236P. 990S-0156467P. 990S-00436430. 990S-0169100P. 99US-0151713P. 27-SEP-1999; 08-NOV-1999; 06-DEC-1999;

The present invention relates to the use or entrymatic autoration calcules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-1b (PTB-IB), methological protein-tyrosine-phosphatase-1b (PTB-IB), methological alpha (PKC alpha), beta-secretase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (BREX/o-erbZ/neu), phospholamban (PLM), presentlin-1 (ps-1), presentlin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-Cleaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-Cleaver, amberzyme, cinclude hammerhead (HH), hairpin, MCH (inozyme), G-Cleaver, amberzyme, cinclude hammerhead (HH), hairpin, MCH (inozyme), G-Cleaver, alsease, clasease, obesity, cardiac disease e.g. heart disease, age-related diseases, bestiffs an interesting cancer, in particular breast cancer, Alzheimer's disease, diseases, obesity, cardiac diseases e.g. heart disease, age-related diseases to be detect the presence acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence cardiace acid molecules can also be used as cardiace represents a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the minimum cardiace associated with them. ö Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease. Gaps 'n present invention relates to the use of enzymatic nucleic acid Chowrira .; 0 DB 5; Length 37; Usman N, Blatt L, Beigelman L, Burgin A; Matulic-Adamic J, Sweedler D, Draper K, Ch Beaudry A, Zinnen S, Lugwig J, Sproat BS; Sequence 37 BP; 6 A; 12 C; 14 G; 0 T; 5 U; 0 Other; Example 4; Page 365; 717pp; English. (RIBO-) RIBOZYME PHARM INC Stinchcomb D, Beaudry A, WPI; 2001-244406/25. Mcswiggen J, Karpeisky A, Query Match

4; Indels 6e+02; , Match
Local Similarity 73.9%; Pred, No. 6e+0
tes 17; Conservative 2; Mismatches 1 CAGCGGAGTGATGGCAAGCACGA 23 Matches RESULT 10

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Human BACE G-cleaver ribozyme seguence #30. 10-FEB-2005 (first entry) ADV04093;

ADV04093 standard; RNA; 37

Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopoptidase; methionine aminopoptidase; meth-2-; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HERZ; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; mepatitis B virus; HBV; hammerhead; HH; hartyni, NCH; inoxyme; G-cleaver; amberzyme; Zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease; diabetes; obesity; cardiac disease; heart disease; age-related disease;

BP.

ADV17630 standard; RNA; 37

(first entry)

10-FEB-2005

ADV17630;

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Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
                                                                                                                                                                                                                                                                          Usman N, Blatt L, Beigelman L, Burgin A;
Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 364; 717pp; English.
                                                                                                               27-SEP-1999; 99US-0046643.
27-SEP-1999; 99US-0046643.
27-SEP-1999; 99US-0156467P.
08-NOV-1999; 99US-00436430.
06-DEC-1999; 99US-00474432.
29-DEC-1999; 99US-00474422.
30-DEC-1999; 99US-00474312.
30-DEC-1999; 99US-00476387.
04-FEB-2000; 2000US-00498824.
20-MAR-2000; 2000US-00531025.
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                                                                                      30-AUG-2000; 2000WO-US023998
                                                                                                                                                                                                                                                         (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                   WPI; 2001-244406/25.
                                                                                                                                                                                                                                                                           Mcswiggen J, U
Karpeisky A, M
Stinchcomb D, 1
                                                 WO200116312-A2.
                              Homo sapiens.
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09-AUG-2000;
                                                                    08-MAR-2001
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The present invention relates to the use of enzymatic muchical actual and cules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-11b (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HER2/c-erb2/neu), phospholamban (PLM) proteins in enzymatic presentlin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, cinclude hammerhead (HH), particular breast cancer, Alzheimer's disease, disease, obesity, cardiac diseases e.g. heart disease, age-related diseases, bepatitis B infections, and hepatitis and hepaticular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased calls and to detect the presence of specific RNA in a cell. The present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
present invention relates to the use of enzymatic nucleic acid
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                                                                                                                                                    Score 16.6; DB 5; Length 37;
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                                                                                                                                                Sequence 37 BP; 9 A; 7 C; 16 G; 0 T; 5 U; 0 Other;
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                                                                                                                                                       6e+02;
                                                                                                                                                       Pred. No. 6e+0
2; Mismatches
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                                                                                                                                                               CAGCGGAGTGATGGCAAGCACGA 23
                                                                                                                                                    69.2%;
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Local Similarity

ઠે 셤 RESULT 11

Query Match Matches

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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (pac-2), and hepatitis B virus (HBW) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, cinzyme, and/or DNazyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diseases, bepatitis B infections, and hepatitis and hepaticcellular carcinoma. The arzymatic uncleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased
                                                        Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta secretase; BACB; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; innoxyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; betast cancer; Alzheimer's disease; diabetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
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Matulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
Human PLN G-cleaver ribozyme sequence #18.
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99US-0169100P.
99US-00474432.
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2000US-0197769P
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99US-0156236P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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Karpeisky A,
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06-DEC-1999;
29-DEC-1999;
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cells and to detect the presence of specific RNA in a cell. The present sequence represents a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 69.2%; Score 16.6; DB 5; Length 37; Best Local Similarity 73.9%; Pred. No. 6e+02; Matches 17; Conservative 2; Mismatches 4; Indels
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Matulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                                                                                Sequence 37 BP; 11 A; 8 C; 11 G; 0 T; 7 U; 0 Other;
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27-SEP-1999;
08-NOV-1999;
06-DEC-1999;
29-DEC-1999;
30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-AUG-2000;
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Karpeisky A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADV04128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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           8\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel{?}{\times}9\stackrel
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Example 4; Page 365; 717pp; English.

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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (MTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HERZ/C-erb2/neu), phospholamban (ELN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HR), hairphin, NCH (inozyme), G-Cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diseases, hepatitis B infections, and hepatitis and hepatitis B infections, and hepatitis and hepatitis and to detect the presence of specific and mutations within diseased diagnostic tools to examine genetic drift and mutations within diseased calls and to detect the presence of specific RNA in a cell. The present sequence represents a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vacchnation; mucokinetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Szymkowski DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5; Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37 BP; 8 A; 10 C; 14 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thompson J, Mcswiggen J, Mckenzie T, Ayers D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human CLCA1 gene enzymatic nucleic acid #3502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 6e+02;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.2%; Score 16.6; 73.9%; Pred. No. 6e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CAGCGGAGTGATGCCAGGACGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCGCAGAGUGAUGGCAUGCACUA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 87; 152pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK59131 standard; RNA; 37 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001; 2001WO-US024970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2000; 2000US-0224383P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SYNT ) SYNTEX USA LLC. (THOM/) THOMPSON J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-217145/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acetylcysteine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK59131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK59131
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The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, cassociated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis; antisense; enzymatic nucleic acid; hammerhead ribozyme; blaxzyme; inozyme; zinzyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative; disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                           69.2%; Score 16.6; DB 6; Length 37; 73.9%; Pred. No. 6e+02; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                          Sequence 37 BP; 8 A; 7 C; 14 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                    enzymatic nucleic acid molecule of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAGCGGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CAGGGUAGUGAUGGCAUGCACUA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virucide; antiinflammatory; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACD53318 standard; RNA; 37 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2001; 2001US-00817879.
08-JUN-2001; 2001US-00877478.
08-JUN-2001; 2001US-0296876P.
24-OCT-2001; 2001US-0335059P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-DEC-2001; 2001US-0337055P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HBV G-cleaver sequence #57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 73.9
Matches 17; Conservative
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MACEJAK D.
MCSWIGGEN J.
MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEE P.
DRAPER K.
ROBERTS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus.
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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(MACE/)
(MCSW/)
(MORR/)
(PAVC/)
(LEEP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DRAP/)
(ROBE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
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The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymes, zinzymes, amberzymes, and G-cleaver ribozymes. DNAzymes, inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase primer sequences, as well care nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV compounds and/or potential therapies directed against HBV, and compounds and/or potential therapies directed against HBV, and compounds and compounds and/or potential therapies directed against HBV, and compounds and compounds and/or potential therapies directed against HBV, and compounds and compounds and without a solution are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepstocellular compounds. The present sequence represents one of the HBV riboxyme, inozyme, G-cleaver, zinzyme, DNAzyme or amberzyme sequences disclosed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                           Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage; hepatitis B virus infection; hepatitis; hepatocellular carcinoma; cirrhosis; liver failure; lamivudine; interferon; genetic drift; virucide; hepatotropic; antiinflammatory; cytostatic.
    Lee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.2%; Score 16.6; DB 8; Length 37; 73.9%; Pred. No. 6e+02; ive 2; Mismatches 4; Indels
  Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis B virus (HBV) enzymatic nucleic acid #1471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37 BP; 8 A; 10 C; 12 G; 0 T; 7 U; 0 Other;
  Mcswiggen J, Morrissey D,
                                                                                                                                                                         Example 1; Page 166; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAGCGGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCCUAGUGAUGGCAUGCACUA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-FEB-1994; 94US-00193627.
08-NOV-1999; 99US-00436430.
20-MAR-2000; 2000US-00531025.
09-AUG-2000; 2000US-00636385.
24-OCT-2000; 2000US-00636347.
08-JUN-2001; 2001US-00877478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JAN-2003; 2003US-00342902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92US-00882712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM61879 standard; RNA; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 73.9'
    Macejak D,
Roberts E;
                                                            WPI; 2003-229207/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2004054156-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAY-1992;
      Blatt L, N
Draper K,
                                                                                                                                         infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM61879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADM61879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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Gaps ; (DRAP/) DRAPER K.

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The invention relates to preparing a double stranded DNA fragment for mutation detection by denaturing high performance liquid chromatography (Dipperighting including during the hybridisation, a nitrogen containing composition (of structure detailed in the specification). The double stranded DNA fragment corresponds to a wild type double stranded DNA fragment having a known nucleotide sequence. The method further comprises: (a) amplifying a section of the double stranded DNA fragment for mutation detection by PCR using a set of primers flanking the section, where at least one primer of the set incorporates a sequence comprising solely GC content on the S' end; (b) hybridising the amplification product of (a) with wild type double stranded DNA corresponding to the section, where a mixture comprising one or more including during the hybridisation, an amount of the nitrogen containing composition. The composition is included to increase the amount of heteroduplex DNA double stranded DNA fragment for mutation detection. Also included are a product of the method above, a kit for preparing a double stranded DNA for mutation detection by liquid chromatography, and containing the hybridish product of the method above, a kit for preparing a double stranded DNA for mutation detection by liquid chromatography, and containing the composition is the method above, a kit for preparing a course of the method above, a kit for preparing a course of the method above, a kit for preparing a course of the method above, a kit for preparing a course of the method above, a kit for preparing a course of the method above, a kit for preparing a course of the method above, a kit for preparing a course of the method above, a kit for preparing a course of the method above, a kit for preparing a course of the method above, a kit for preparing a course of the method above, a kit for preparing a course of the method above, a kit for preparing a course of the method above, a kit for preparing a course of the method above, a kit for preparing a c
            denaturing high performance liquid chromatography, comprises including during hybridization composition comprising a nitrogen-containing organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresponding to the target sequence, and a kit for analysing a double stranded DNA for mutation detection by liquid chromatography. The method is useful for preparing a double stranded DNA fragment for mutation analysis, and for diagnosing a disease. The method improves the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resolution between hereroduplex and homoduplex peaks even for mutations that are difficult to detect. The present sequence is a PCR primer used to amplify variants of the human Y chromosome locus DYS271 (which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single nucleotide polymorphisms) and is used to demonstrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone cGMP-5 for allosteric modulation of hammerhead ribozyme by cGMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hammerhead ribozyme; molecular sensor; signalling agent; ligand; FMN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          flavin mononucleotide; conformational change; molecular switch; CM; communication module; allosteric; sensing element; environmental; agricultural; clinical; industrial; genetic control; cGMP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.3%; Score 16.4; DB 10; Length 45; 70.8%; Pred. No. 7.6e+02; ive 3; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/label= Communication_module
/note= "Comprises substitution mutations"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        b
"Cytosine substituted with Uracil"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45 BP; 8 A; 11 C; 14 G; 7 T; 0 U; 5 Other;
                                                                                                                                  Example 4; SEQ ID NO 4; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGMTGMGTGMTGGCATACAGGAC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAGCGGAGTGATGGCAAGCACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 70.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD00496 standard; RNA; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
                                                                          compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 17
AAD00496
            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE STATE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an enzymatic nucleic acid molecule that expecifically cleaves RNA derived from hepatitis B virus (HBV) and comprising one or more binding arms, without requiring the presence of a 2'-0H group within the molecule for activity. The nucleic acids are useful for treating hepatitis B virus infection, hepatitis, hepatocellular carcinoma, cirrhosis and liver failure, either alone combination with other therapies such as lamivudine and interferons. The nucleic acids are useful as diagnostic tools to examine genetic drift and mutations within diseased cells, for detecting the presence of HBV RNA in a cell, for the study of RNA and for down-regulating gene expression of target genes in bacterial, fungal, viral, plant or mammalian cells. This sequence represents an enzymatic nucleic acid molecule which cleaves HBV RNA of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                           Novel enzymatic nucleic acid molecule such as DNAzymes and inozymes specifically cleaving RNA derived from hepatitis B virus and comprising one or more binding arms, useful for treating hepatitis and cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, Y chromosome, DYS271; SNP; single nucleotide polymorphism; 88;
mutation detection; denaturing high performance liquid chromatography;
DHPLC; nitrogen containing composition; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Preparing a double stranded DNA fragment for mutation detection by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.2%; Score 16.6; DB 12; Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human locus DYS271 30C-44A-168A variant PCR primer #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37 BP; 8 A; 10 C; 12 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                            Morrissey D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 6e+0
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 4013; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CAGCCUAGUGAUGGCAUGCACUA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAGCGGAGTGATGGCAAGCACGA 23
                                                                                                                            Mcswiggen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-2001; 2001US-00033104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0244436P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 73.9%;
les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC33588 standard; DNA; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                  MCSWIGGEN J A.
MORRISSEY D.
                                                                                                                        Blatt L,
                                                                                                                                                                                WPI; 2004-247781/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-743884/70.
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(BLAT/) BLATT L.
(MCSW/) MCSWIGGEN
(MORR/) MORRISSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003082557-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-OCT-2000;
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                                                                                                                            Draper K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taylor PD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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Gaps

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Human; 88; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; dearer; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; parkinson's disease; ataxia; Huntington's disease; substrate sequence; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

Human NOGO G-Cleaver substrate sequence #29.

(first entry)

12-MAR-2002

ABK05366;

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constructed using harmmerhead ribozyme RNAs, comprising a actuator or catalytic domain, bridging domain and receptor or aptamer domain. The interaction of the receptor with a signalling agent like a ligand e.g., flavin mononuclectide (FMN) or physical signal, triggers a conformational change in the bridging domain, that modulates the catalytic or reporter activity of the actuator domain. If functions as a molecular switch.

Communication module (CM) sequences can be inserted as the bridging domain, that enhances the allosteric properties. The ligand-specific sensors may be used as sensing elements in clinical, agricultural, industrial and environmental analyses and as genetic control or reporter elements for the regulation of gene expression. The present RNA sequence is the clone cGMP-5, isolated from G18' RNA population, after selective is the clone cGMP-5, isolated from G18' RNA population, after selective mammerhead ribozymes by cGMPs. This clone comprises mutations in the hammerhead ribozymes by cGMPs. This clone comprises mutations in the appramer domain (deletions) and communication module (substitutions)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel functional polynucleotides comprising an actuator domain, a receptor domain, and a bridging domain useful for generating highly specific polynucleotide sensors and as genetic control elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The patent discloses multidomain polynucleotide molecular sensors,
                                                                                                                                                                                                                                                                 *tag= h
note= "Guanine substituted with Cytosine"
                                                                                                                                                                                                                 *tag= g
note= "Cytosine substituted with Adenine"
                                                                                          '*tag= e
|aabel= Communication_module
'note= "Comprises substitution mutations"
                                                                                                                                                                            note= "Adenine substituted with Uracil"
                                                                                                                                                                                                                                                                                                                       /*tag= i
/note= "Uracil substituted with Guanine"
"Uracil substituted with Guanine"
                                     d
"Corresponds to aptamer domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32 BP; 7 A; 8 C; 11 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Fig 10A; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US025497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0106829P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0126683P
                                                                        29. .32
                    . .28
*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GA;
                                                                                                                                                               *tag=
                                                         note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-365558/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soukup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                            WO200026226-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-1999;
                      misc_feature
                                                                        misc_feature
                                                                                                                                              misc_feature
                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Breaker RR,
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11-FEB-2000; 2000US-0181797P. 28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P.

RIBOZYME PHARM INC.

(RIBO-)

BLATT L. MCSWIGGEN J. CHOWRIRA B M.

(BLAT/) (MCSW/) (CHOW/)

09-FEB-2001; 2001WO-US004273

WO200159103-A2 Homo sapiens. Synthetic.

16-AUG-2001.

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expression of a nucleic acid molecule which down captures or a mucleic acid molecule which down captures or a C2020 gene and a nucleic acid molecule which down captures acypression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acid cleaving a an RNA molecule possessing an NCH motif), a G-cleaving RNA with a NYN motif) prossessing an NCH motif), a G-cleaving RNA with a NYN motif) prossessing an NCH motif). The CD20-targetting nucleic acid is used to cleaving RNA with a vGY motif). The CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably MG'2+.

CC Furthermore, it may be contacted with a cell to reduce CD20 activity of the call and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more the call and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more the call and treatment, becall lymphoma, low-grade or follicular nn. CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular nn. CC treat lymphoma (MCL), immunocytoma (MC), small B-cell lymphocytic lymphoma (MCL), immunocytoma (MC), small B-cell lymphocytic lymphoma (MCL), immunocytoma (MC), small B-cell lymphocytic lymphoma (MC), immunocytoma (MC), small B-cell lymphocytic cargetting nucleic acid as used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably MG'2+. Furthermore, the condition associated with the level of cell and treat a patient having a condition associated with the level of cell and treat a patient having a condition associated with the level of the call and treat a patient having a condition associated with the level of the treatment may further comprise the use of one or more thereafted the nogo-targetting nucleic acid may be used to cleave RNA of the use of one or more cell therapies. In particular, the NOGO-targetting nucleic acid may be used to cleave 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to a nucleic acid molecule which down regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 89; Page 92; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               central nervous system injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-607195/69.
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Gaps

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3; Indels

Score 16.2; DB 3; Pred. No. 9.1e+02; 1; Mismatches 3;

67.5%; 81.0%;

Local Similarity 81.0 es 17; Conservative

datches

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Query Match

22

AGCGGAGCGAUGGCAGCCACG 28

ABK05366 standard; RNA; 37 BP

RESULT 18 ABK05366

Length 32;

Chowrira BM;

Mcswiggen J,

Blatt L,

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Example 6; Page 531; 717pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 3 GCGGAGTGATGGCAGGA 23
                                                                                                                                                                                                                                                                                                                                                                                                3 GCCGAGUGAUGGCAUGCACUA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK20721 standard; RNA; 37 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAY-2001; 2001WO-US015866.
                                                                                                                                                                                                                                                                                                                                    67.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAY-2000; 2000US-00572021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Von Carlowitz I,
                                                                                                                                                                                                                                                                                                                                              76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-2002 (first entry)
     obesity and heart disease.
                                                                                                                                                                                                                                                                                                                                                           16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-082995/11.
                                                                                                                                                                                                                                                                                                                                              Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200188124-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amberzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jarvis T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK20721;
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK20721
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                                                                                                                                                                                                                                                                                                                                                                  Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberzyme; zinzyme; cancer; breast cancer; Alzheimer's disease; disbetes; obesity; cardiac disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; ss.
treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease setates which respond to the modulation of NOGO expression. The present sequence is a substrate sequence for a nucleic acid of the invention based on the human NOGO sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
                                                                                                                                                              Gaps
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                                                                                                                                                              ..
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                                                                                                                                    Score 16.2; DB 4; Length 37; Pred. No. 9.2e+02;
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Sweedler D, Draper K, Ch
1 S, Lugwig J, Sproat BS;
                                                                                                                                                             3; Indels
                                                                                                             Sequence 37 BP; 6 A; 8 C; 18 G; 0 T; 5 U; 0 Other;
                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beaudry A, Zinnen S,
                                                                                                                                                                                                                                                                                                                                             HBV G-cleaver ribozyme sequence #41.
                                                                                                                                                                                   3 GCGGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                 3 GGGGAGUGAUGGCAUGCACUA 23
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Matulic-Adamic J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-AUG-1999; 99US-0151713P.
27-SEP-1999; 99US-016643.
27-SEP-1999; 99US-0156467P.
08-NOV-1999; 99US-0156467P.
08-DC-1999; 99US-00436430.
29-DEC-1999; 99US-00476312P.
29-DEC-1999; 99US-00476387.
04-FEB-2000; 2000US-00531025.
                                                                                                                                      67.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                      ADV47946 standard; RNA; 37
                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                           16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-244406/25.
                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200116312-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stinchcomb D,
                                                                                                                                                                                                                                                                                                                      10-FEB-2005
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Karpeisky A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAR-2001
                                                                                                                                                                                                                                                                                              ADV47946;
                                                                                                                                                             Matches
                                                                                                                                                                                                                                                 RESULT 19
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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor ceptor-2 (HERA/C-erb2/neu), phospholaban (PLM), presentlin-1 (ps-1), presentlin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucled hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Altheimer's disease, diabetes, obesity, cardiac diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presente of specific RNA in a cell. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Randi AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mclaughlin F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16.2; DB 5; Length 3. Pred. No. 9.2e+02; 2; Mismatches 3; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37 BP; 7 A; 8 C; 14 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ERG G-cleaver ribozyme, Seg ID No 3368.
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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, cumour angiofibroma of tubbarcous sclerosis, port-wine stains, Sturge weber syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. Leukaemia or tumour conditions suitable for the treatment. Leukaemia or tumour conditions suitable for the treatment. Leukaemia or tumour conditions with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or cell, by contacting (I) is useful for reducing ERG activity in a cc. ell, by contacting (I) with RN, in the presence of a divalent cation such as Mg2+. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to targeting genes that share homology with ERG gene or ERG fusion genes. ABK17354-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and centared PCR primers of the invention
Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis; antisense; enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degemerative, disease state, HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; virucide; antiinflammatory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.5%; Score 16.2; DB 6; Length 37; 76.2%; Pred. No. 9.2e+02; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37 BP; 7 A; 10 C; 12 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GCGGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GCGUAGUGAUGGCAUGCACUA 23
                                                                                                    Claim 5; Page 82; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACD53251 standard; RNA; 37 BP
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08-JUN-2001; 2001US-00877478.
08-JUN-2001; 2001US-0296876P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HBV G-cleaver sequence #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-SEP-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200281494-A1.
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The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enviranter nucleic acids such as hammerhead ribozymes. DNAzymes, concerning an environment, amberzymes, amberzymes, and enzymes. Also disclosed inozymes, zinzymes, amberzymes, and g-cleaver ribozymes. BNAzymes, concerning as oligonucleotides that specifically bind the Enhancer I region of HBV compounds and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents one of the HBV ribozyme, incorning in prayme, G-cleaver, zinzyme, DNAzyme or amberzyme sequences disclosed in
                                                                                                                                                                                                                                                                                            Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                              .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage; hepatitis B virus infection; hepatitis; hepatocellular carcinoma; cirrhosis; liver failure; lamivudine; interferon; genetic drift; virucide; hepatotropic; antiinflammatory; cytostatic.
                                                                                                                                                                                                              Lee
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                                                                                                                                                                                                              Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis B virus (HBV) enzymatic nucleic acid #1455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37 BP; 7 A; 8 C; 14 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                              Mcswiggen J, Morrissey D,
                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 165; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GCCGAGUGAUGGCAUGCACUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GCGGAGTGATGGCAAGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM61863 standard; RNA; 37 BP
24-OCT-2001; 2001US-0335059P.
05-DEC-2001; 2001US-0337055P.
                                               RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 76.2
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the present invention
                                                                                                                                                                                                                Macejak D,
Roberts E;
                                                                            MACEJAK D.
MCSWIGGEN J.
MORRISSEY D.
                                                                                                                                                                                                                                                               WPI; 2003-229207/22.
                                                                                                                                                                                 ROBERTS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus
                                                                                                                                                 LEE P.
DRAPER K.
                                                                                                                                 PAVCO P.
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                                                                                                                                                                                                                 Blatt L, M
Draper K,
                                                                                                                                                                                                                                                                                                                                     infection.
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                                                               (BLAT/) E
(MACE/) N
(MCSW/) N
(MORR/) N
(PAVC/) E
(LEEP/) I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                 (ROBE/)
                                                 (RIBO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
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us-10-713-137-2.sizlim.rng

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The invention relates to antisense compounds, especially

Oligonuclectides, which are targeted to a nucleic acid encoding inducible

intric oxide synthase and which specifically hybridise to and modulate

expression of inducible nitric oxide synthase. The antisense compounds

have immunomodulator, antidiabetic, cardiovascular, cardiant,

cardiovascular, cardiant,

cardiovascular, cardiant,

coligonucleotides are useful for inhibiting the expression of inducible

coligonucleotides are useful for inhibiting the expression of inducible

coligonucleotides are useful for trissues. In particular, the antisense

coligonucleotides are useful for treating diseases or disorders associated

with inducible nitric oxide synthase, e.g. diabetes immunological

cischaemia/reperfusion injury. The antisense oligonucleotides are also

cuseful for research and disorder. The present sequence is that of an

cuseful for research and diagnostics. The present sequence is that of an

cuseful for research and diagnostics. The present

cuseful for research and diagnostics. The present

cuseful for research and diagnostics. The present

cuseful for research and something appeare oligonucleotide with a

cuseful for rucleotide 2'-MOE (2'-methoxytethyl) wings (cytidine

creaidues in the 2'-MOE wings are 5-methylyctidines) and targeted to human

custules in the 2'-MOE wings are 5-methylycytidines) and targeted to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                  /note= "phosphorothioate backbone, 5' and 3' four nucleotide 2'-MOE (2'-O-methoxyethyl) wings (the cytidine residues in the 2'-MOE wings are 5-methylcytidines) and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense oligonucleotides for modulating the expression of inducible nitric oxide synthase in cells or tissues, particularly useful for treating e.g. immunological, cardiovascular or neurological disorders, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; hetAP-2; human telomerase; hTERT; protein kinase c alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 1e+03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti human MetAP-2 G-cleaver ribozyme sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 4 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 15; Page 83; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.,',
100.0%; Pre-
0, }
/*tag= a
/mod base= OTHER
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                                                                                                                                                                                deoxy gap"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
1es 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bennett CF, Dean NM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-465340/50.
                                                                                                                                                                                                                                                      WO200152902-A1
                                                                                                                                                                                                                                                                                                                         26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADU85578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an enzymatic nucleic acid molecule that specifically cleaves RNA derived from hepatitis B virus (HBV) and comprising one or more binding arms, without requiring the presence of a 2.0H group within the molecule for activity. The nucleic acids are useful for treating hepatitis B virus infection, hepatitis, hepaticis, hepatocilular carcinoma, cirrhosis and liver failure, either alone or in combination with other therapies such as lamivudine and interferons. The nucleic acids are useful as diagnostic tools to examine genetic drift and mutations within diseased cells, for detecting the presence of HBV RNA in a cell, for the study of RNA and for down-regulating gene expression of target genes in bacterial, fungal, viral, plant or mammalian cells. This sequence represents an enzymatic nucleic acid molecule which cleaves HBV RNA of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel enzymatic nucleic acid molecule such as DNAzymes and inozymes specifically cleaving RNA derived from hepatitis B virus and comprising one or more binding arms, useful for treating hepatitis and cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense oligonucleotide; inducible nitric oxide synthase; NOS; modulate expression; immunomodulator; antidiabetic; cardiovascular; cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury; 2'-O-methoxyethyl; phosphorothioate; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human inducible NOS antisense oligonucleotide SEQ ID NO 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37 BP; 7 A; 8 C; 14 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcswiggen JA, Morrissey D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 3997; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GCGGAGTGATGGCAAGCACGA 23
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                                                                                                                                        92US-00882712.
94US-00193627.
99US-00436430.
2000US-00531025.
2000US-00636385.
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                                                                                                                                                                                                                                                                                                                     24-OCT-2000; 2000US-00696347
08-JUN-2001; 2001US-00877478
                                                                      15-JAN-2003; 2003US-00342902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCSWIGGEN J A. MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blatt L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-247781/23
                                                                                                                                                                                                                                                                                                                                                                                                                                DRAPER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
modified base
                                                                                                                                        14-MAY-1992;
07-FEB-1994;
08-NOV-1999;
                                                                                                                                                                                                                                               20-MAR-2000;
09-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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   18-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Draper K,
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(MORR/)
                                                                                                                                                                                                                                                                                                                                                                                                                            DRAP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLAT/)
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2 GGAGUGAUGGCAUGCACUA 20

BP.

ADU94721 standard; RNA; 36

RESULT 25 ADU9472 Human TERT G-cleaver ribozyme sequence #143.

(first entry)

10-FEB-2005

ADU94721;

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WPI; 2001-244406/25.
                       WO200116312-A2
                                                                                                 Stinchcomb D,
                                                                                           Mcswiggen J,
                  Homo sapiens.
                                                          29-DEC-1999;
29-DEC-1999;
30-DEC-1999;
                                                                   04-FEB-2000;
                                                                       20-MAR-2000;
                                                                               09-AUG-2000;
                                                                          14-APR-2000;
                                                                            23-MAY-2000;
                                                                                               Karpeisky A,
                                                 27-SEP-1999
08-NOV-1999
                                                        06-DEC-1999
                             08-MAR-2001
                                               27-SEP-1999
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anso methicus to the first was to use a replacate of first. The expression of aminopeptidase (MetAP-2), human telomerase (HTB-T), protein kinase C alpha (PKC alpha), beta-secretase (BACB), human epidermal growth factor receptor-2 (HER2/c-er22/neu), phospholamban (PLN), presentlin-1 (ps-1), presentlin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammarhead (HH), haripin, NCH (inczyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diabetes, obseity, cardiac diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic difft and mutations within diseased calls and to detect the presence of specific NNA in a cell. The present sequence represents an anti human ribozyme used in the examples of the bream to the specification, but these have different sequences associated with
hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; anaberzyme; anaberzyme; anaberzyme; anaberzyme; adiaberae; alzaheimer's disease; diabetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usman N, Blatt L, Beigelman L, Burgin A;
Matulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 36 BP; 8 A; 6 C; 13 G; 0 T; 9 U; 0 Other;
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99US-0156236P.
99US-0156467P.
99US-010436430.
99US-0164432.
99US-0173612P.
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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention gens also methods for their use to down regulate or inhibit the expression of gense encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBR), protein kinase C alpha) (PKC alpha), beta-secretase (BACB), human epidermal growth factor receptor-2 (HERZ/c-erb2/neu), phospholamban (PLM), presentiln-1 (ps-1), presentiln-2 (ps-2), and hepstitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), g-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease,
                                                                                         Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; heath-2. human tedomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HERZ; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inoxyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; beast cancer; Alzheimer's disease; diabetes; obesity; cardiac disease; heatt disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
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Chowrira B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Draper K, Ch
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Sweedler D, Dre
n S, Lugwig J,
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Matulic-Adamic J, Swee
Beaudry A, Zinnen S,
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                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0151713P.
99US-00406643.
99US-0156236P.
99US-0156467P.
99US-0163100P.
99US-0163100P.
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Karpeisky A, Ma
Stinchcomb D, I
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                                                                                                                                                                                                                                                                                       Homo sapiens.
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29-DEC-1999;
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GGAGTGATGGCAAGCACGA 23

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Gaps

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65.8%; Score 15.8; DB 5; Length 36; 78.9%; Pred. No. 1.4e+03; Live 2; Mismatches 2; Indels

Query Match Best Local Similarity 78.9 Matches 15; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; HTERT; protein kinase Calpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; beast cancer; Alzheimer's disease; disbetes; obesity; cardiac disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
diabetes, obseity, cardiac diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
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                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                    65.8%; Score 15.8; DB 5; Length 36; 78.9%; Pred. No. 1.4e+03;
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Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Ch
Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                        2; Indels
                                                                                                                                                     Sequence 36 BP; 8 A; 9 C; 13 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human TERT G-cleaver ribozyme sequence #266.
                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                       5 GGAGTGATGGCAAGCACGA 23
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99US-00406643.
99US-0156236P.
99US-015647P.
99US-00436430.
99US-00474432.
99US-0173612P.
99US-0173612P.
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14-APR-2000; 2000US-0197769P.
23-MAY-2000; 2000US-00578223.
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                                                                                                                                                                                                                                                                                                                                                                        ADU94968 standard; RNA; 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                      15; Conservative
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                                                                                                                                                                                      Query Match
Best Local Similarity
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29-DEC-1999;
30-DEC-1999;
04-FEB-2000;
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27-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                         ADU94968;
                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                           RESULT 26
     8X33333333X8
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The present invention relates to the use of enzymatic nuclear action also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (hTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), protein kinase C presentiin-2 (ps-2), and hepatitis B virus (HBN) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful cor treating cancer, in particular breast cancer, Alzheimer's disease, diabetes, obesity, cardiac disease s.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as a calcinoma. The present cancer of specific RNA in a cell. The present cancer a ribory in the examples of the present cancer and the present cance
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are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them
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                                                                                                                                                                                                              present invention relates to the use of enzymatic nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.8; DB 5; Length 36; Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36 BP; 7 A; 11 C; 12 G; 0 T; 6 U; 0 Other;
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                                                                                                                        Example 1; Page 307; 717pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 GGAGTGATGGCAAGCACGA 23
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99US-0156236P.
99US-0156467P.
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99US-0169100P.
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78.9%;
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nes 15; Conservative
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08-NOV-1999;
06-DEC-1999;
29-DEC-1999;
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99US-0169100P. 99US-00474432. 99US-0173612P.

99US-00476387 2000US-00498824

99US-00436430

2000US-00531025 2000US-0197769P

2000US-00578223 2000US-00636385

99US-00406643. 99US-0156236P. 99US-0156467P.

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30-AUG-2000; 2000WO-US023998
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                                                                                                                                                                                                                                                            27-SEP-1999;
08-NOV-1999;
06-DEC-1999;
29-DEC-1999;
30-DEC-1999;
                                           Homo sapiens.
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20-MAR-2000;
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23-MAY-2000;
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                                                                                                                        08-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACB), human epidermal growth factor receptor-2 (HERZ/c-erbZ/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-Claever, amberzyme, include hammerhead (HH), hairpin, NCH (inozyme), G-Claever, amberzyme, cinclude hammerhead (HH), particular breast cancer, Alzheimer's disease, disease, age-related diseases, hepatitis B infections, and hepatitis and hepaticcellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cals and to detect the presence of specific RNA in a cell. The present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
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                                                                                                                                                                                                                                                                                                                                    Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
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Matulic-Adamic J, Sweedler D, Draper K, Chowrira
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36 BP; 6 A; 9 C; 15 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PTP-1B G-cleaver ribozyme sequence #110.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADM90363 standard; RNA; 36 BP
                                         04-FEB-2000; 2000US-00498824.
20-MAR-2000; 2000US-00531025.
14-APR-2000; 2000US-0197769P.
23-MAY-2000; 2000US-00578223.
09-AUG-2000; 2000US-00636385.
  99US-0173612P.
                                                                                                                                                                    (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                             WPI; 2001-244406/25.
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                                                                                                                                                                                                           Mcswiggen J, Us
Karpeisky A, Ma
Stinchcomb D, E
    29-DEC-1999;
30-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 28
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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-Cleaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-Cleaver, amberzyme, cardiac diseases e.g. heart disease, age-related diseases, obesity, cardiac diseases e.g. heart disease, age-related diseases, bepatitis B infections, and hepatitis and hepaticis and hepaticis and hepatitis and codecet the presence of specific and mutations within diseased calbin and to detect the presence of specific RNA in a cell. The present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
                                                                                                                                                                                                                                                    Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
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Usman N, Blatt L, Beigelman L, Burgin A;
Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36 BP; 8 A; 5 C; 15 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 211; 717pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGAGUGAUGGCAUGCACUA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 GGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Conservative
                                                                                                                                                                                         WPI; 2001-244406/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                      Karpeisky A, P
Stinchcomb D,
                  Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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RESULT 29 ADU85545

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Example 2; Page 211; 717pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACB), human epidermal growth factor receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presentin-1 (ps-1), presentin-2 (ps-2), and hepatitis B virus (HBV) proteins. The maxymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inoxyme), G-claver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Albrieimer's disease, diabetes, obesity, cardiac disease e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular cardinage includes can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presente of specific RNA in a cell. The present
                                                                                                                                                                        Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase Calpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; mepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inoxyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; branchimer's disease; diabetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
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Matulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                   Human MetAP-2 G-cleaver ribozyme substrate sequence #133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 264; 717pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-AUG-1999; 99US-0151713P.
27-SEP-1999; 99US-00406643.
27-SEP-1999; 99US-0156256P.
27-SEP-1999; 99US-0156467P.
08-NOV-1999; 99US-01646130.
29-DEC-1999; 99US-01474432.
29-DEC-1999; 99US-0173612P.
30-DEC-1999; 99US-0173612P.
30-DEC-1999; 99US-0173612P.
30-DEC-1999; 99US-0173612P.
30-DEC-1999; 99US-0173612P.
30-MAR-2000; 2000US-0197769P.
23-MAY-2000; 2000US-0197769P.
  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000WO-US023998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2000; 2000US-00636385
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ADU85545 standard; RNA; 36
                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-244406/25.
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Karpeisky A, M
Stinchcomb D,
                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-AUG-2000;
                                                                                         10-FEB-2005
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                                           ADU85545;
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
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sequence represents a substrate/target sequence for a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACB; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inoxyme; G-cleaver; amberzyme; zinzyme; Daxyme; cancer; beast cancer; Alzheimer's disease; diabetes; obesity; cardiac disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä
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Matulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                 Length 36;
                                                                                                                                                                                                                               Indels
                                                                                                                             Sequence 36 BP; 8 A; 6 C; 13 G; 0 T; 9 U; 0 Other;
                                                                                                                                                                            Score 15.8; DB 5;
Pred. No. 1.4e+03;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PTP-1B G-cleaver ribozyme sequence #108.
                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                5 GGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                              2 GGAGUGAUGGCAUGCACUA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM90361 standard; RNA; 36 BP.
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99US-00436430.
99US-0169100P.
99US-00474432.
                                                                                                                                                                              65.8%;
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99US-0156236P.
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2000US-00578223
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99US-00476387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-FEB-2005 (first entry)
                                                                                                                                                                            Query Match
Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-244406/25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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Karpeisky A,
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08-NOV-1999;
06-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-APR-2000;
23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADM90361;
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 30
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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MELAP-2), human telomerase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HER2/c-er2/neu), phospholamban (PLM), presentlin-1 (ps-1), presentlin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammarhead (HH), hairpin, NCH (inczyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diseases, hepatitis B infections, and hepatitis and hepatitis and hepatitis and hepatitis and hepatitis and diseased diseases, hepaticis B infections, and hepatitis and mutations within diseased diseases, hepaticis a became genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a ribozyme used in the examples of the present interperture and mutation. When the present interpeted more than once in the parameter of the present interpeted more than once in the present interpeted more than once in the present interpeted more present interpeted more in the present interpeted more interpeted mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification, but these have different sequences associated with them.
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les 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200116312-A2.
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Matches
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Gaps ..

2; Indels

2; Mismatches

Score 15.8; DB 5; Length 36; Pred. No. 1.4e+03;

65.8%;

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Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; meth-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; new; phospholamban; PKI; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberzyme; vlaxyme; DMAxyme; cancer; breast cancer; Alzheimer's disease; disbetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
                                                                                    Human TERT G-cleaver ribozyme sequence #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     990S-0169100P.
990S-00474432.
990S-0173612P.
99US-00476387.
2000US-00498824.
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99US-00406643.
99US-0156236P.
99US-0156467P.
99US-00436430.
ADU94468 standard; RNA; 36 BP
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                                                         (first entry)
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04-FEB-2000;
20-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-1999;
27-SEP-1999;
08-NOV-1999;
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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBAT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (IERZ/O-erbZ/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-Cleaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-Cleaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-Cleaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-Cleaver, amberzyme, cardiac diseases e.g. heart disease, age-related diseases, besity, cardiac diseases e.g. heart disease, age-related diseases, besity, cardiac diseases e.g. heart disease, age-related diseases, bepatitis B infections, and hepatitis and hepaticis and hepatitis and colect the presence of specific and mutations within diseased calsianostic tools to examine genetic drift and mutations within diseased calsianostic rools to examine genetic drift and mutations within diseased calcuments a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
                                                                                                                                                                                                                                    Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
                                                                                                                                      Chowrira B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.8; DB 5; Length 36;
Pred. No. 1.4e+03;
2; Mismatches 2; Indels
                                                                                                                                      Matulic-Adamic J, Sweedler D, Draper K, Ch.
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                     Burgin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36 BP; 6 A; 9 C; 15 G; 0 T; 6 U; 0 Other;
                                                                                                                       Beigelman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Chkl ribozyme SEQ ID NO: 2138.
                                                                                                                                                                                                                                                                                                                     Example 1; Page 299; 717pp; English.
                                                                                                                     Blatt L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGAGUGAUGGCAUGCACUA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 GGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH96713 standard; RNA; 37 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-FEB-2001; 2001WO-US003504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-FEB-2000; 2000US-0179983P
14-APR-2000; 2000US-0197769P.
23-MAY-2000; 2000US-00578223.
09-AUG-2000; 2000US-00636385.
                                                                               (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity 78.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA cleavage; cancer; ss.
                                                                                                                                                                                                    WPI; 2001-244406/25.
                                                                                                                       Mcswiggen J, Ul
Karpeisky A, Ma
Stinchcomb D, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157206-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH96713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH96713
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The invention relates to a nucleic acid molecule which down regulates expression of a cutto and a nucleic acid molecule which down control and a nucleic acid molecule which down control and a nucleic acids (e.g. a ribozyme or a nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acid cleaving an RNA molecule possessing an NCH motifi), a G-cleaver (cleaving RNA with a NVR) motifi) proposessing an NCH motifi), a G-cleaver (cleaving RNA with a NVR) motifi) proposessing an NCH motifi), a G-cleaver (cleaving RNA with a NVR) motifi) proposessing an NCH motifi), and G-cleaver (cleaving RNA with a NVR) motifi) proposes (cleaving RNA with a NVR) motific a cid divalent cation that is preferably MG<sup>2</sup>+.

Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of fone or more checken is, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (MHL), small B-cell lymphocytic lymphoma, immunocytoma (MHL), small B-cell lymphocytic lymphoma, compacted vith a cell to reduce NOGO gene in the presence of a divalent cation that is preferably Mg<sup>2</sup>+. Furthermore, the contacted with a cell to reduce NOGO gene in the presence of a divalent cation that is preferably Mg<sup>2</sup>+. Furthermore, the condition associated with the level of concleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg<sup>2</sup>+. Furthermore, the conclain cation that is preferably Mg<sup>2</sup>+. Furthermore, the conclain cation that is preferably Mg<sup>2</sup>-+. Furthermore, the coll and treat a patient having a condition associated with the level of the condition associated with the level of chearges. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CNA, stroke), Allahamer's disease, dementia, muscular disea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOG0; hammerhead ribozyme; DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lumphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
                                                                                   Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructe, which down regulate expression of a CD20 gene or neuxite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence is a substrate sequence for a nucleic acid of the invention based on the human NOGO sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.8%; Score 15.8; DB 4; Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37 BP; 11 A; 6 C; 13 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.4e+03;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human CD20 G-Cleaver substrate #34.
                                                                                                                                                                                                                                  Claim 89; Page 93; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 GGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGUGAUGGCAUGCACUA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK08475 standard; RNA; 37 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
                             WPI; 2001-607195/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sest Local Similarity
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ABK08475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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                                                                                                                                                                                                                                                                                                                                                                        The present invention provides nucleic acid molecules capable of downregulating the expression of the human checkpoint kinase-1 (Chkl) gene. These may be antisense or ribozyme sequences, and are useful in the treatment of diseases associated with conditions affected by Chkl levels, including cancer. The present sequence is an oligonucleotide described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; se; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NGC0; hammerhead ribozyme; DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; Jymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; Muman immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amsotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; substrate sequence; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
                                                                                                                                                                                                 Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid molecules, which downregulates expression of a checkpoint kinase-1 gene, useful for treating colorectal, lung, breast or prostate cancers.
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                                                                                         Booher RN, Holman PS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.8%; Score 15.8; DB 4; Length 37; 78.9%; Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37 BP; 9 A; 7 C; 11 G; 0 T; 10 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human NOGO G-Cleaver substrate sequence #90.
                                                                                         Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chowrira BM;
                                                                                                                                                                                                                                                                                                                         Claim 5; Page 67; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GGAGUGAUGGCAUGCACUA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 GGAGTGATGGCAAGCACGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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     RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK05427 standard; RNA; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 78.5.
These 15; Conservative
                                                                                      Jarvis T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHOWRIRA B M.
(RIBO-) RIBOZYME PHA
(FATT/) FATTAEY A R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLATT L.
MCSWIGGEN J.
                                                                                                                                               WPI; 2001-496922/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200159103-A2.
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28-FEB-2000;
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                                                                                         Fattaey AR,
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ABK05427;

RESULT 33 ABK05427

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MCSW/) CHOM/) BLAT/)

Homo

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Gaps

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down cregulates expression of a neurite growth inhibitor gene (NGGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NCW nuclei) a zinzyme (cleaving RNA with an NCW triple), a zinzyme (cleaving RNA with an NCW triple), a zinzyme (cleaving RNA with an NCW triple), a zinzyme (cleaving RNA with an VCW motif). The CD20-targetting nucleic acid is used to cleave RNA cc of CD20 in the presence of a divalent cation that is preferably MG²+. Creatment in the cell and treat a patient having a condition associated with the level cc for CD20. The treatment may further comprise the use of one or more treat lymphoma, leukaemia, HCW claragetting nucleic acid may be used to treat lymphoma (MCL), immunocytoma [NCO] lymphoma, low-grade or follicular nontrapted may (MCL), immunocytoma (NC), small B-cell lymphocytic lymphocytic lymphocytic creat caid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that a preferably MG²+. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of coll and treat a patient having a condition associated with the level of therapies. In particular, the NOGO-targetting nucleic acid may be used to cleave RNA of the ore or more coll and treat a patient divalent acomprise the use of one or more therapies. In particular, the NOGO-targetting nucleic acid may be used to charge contacted with a cell to reduce NOGO activity of the creat central nervous system (CNA) intro comprise the use of one or more therapies. In particular, and interact of deman and patient may further comprise the use of one or more contacted may entered the nucleof chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; substrate sequence; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease. Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The presensequence is a substrate sequence for a nucleic acid of the invention based on the human CD20 sequence Chowrira BM; Claim 31; Page 152; 200pp; English. central nervous system injury. 11-FEB-2000; 2000US-0181797P. 28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P. 09-FEB-2001; 2001WO-US004273 RIBOZYME PHARM INC Mcswiggen J, BLATT L. MCSWIGGEN J. CHOWRIRA B M. WPI; 2001-607195/69. 40200159103-A2. 16-AUG-2001 Synthetic. Blatt L,

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Length 37;
Sequence 37 BP; 6 A; 8 C; 12 G; 0 T; 11 U; 0 Other;
                                       65.8%; Score 15.8; DB 4; 78.9%; Pred. No. 1.4e+03;
                                                     Local Similarity
                                           Query Match
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; 0

Gaps

; 0

2; Indels

2; Mismatches

The present

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Human, chloride channel calcium activated 1, CLCA1, ss; antiasthmatic; antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
                                                                                                                                                                                                                                                                                                                                                                                               Ensymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.
                                                                                                                                                                                                                                                                                                                                               Szymkowski DE;
                                                                                                                                                                                                                                                                                                                                                Mcswiggen J, Mckenzie T, Ayers D,
                                                                                                                     Human CLCA1 gene enzymatic nucleic acid #3492.
5 GGAGUGAUGGCAUGCACUA 23
                                                             ABK59121 standard; RNA; 37 BP
                                                                                                                                                                                                                                                                  09-AUG-2001; 2001WO-US024970.
                                                                                                                                                                                                                                                                                      09-AUG-2000; 2000US-0224383P.
                                                                                                                                                                                                                                                                                                        (RIBO-) RIBOZYME PHARM INC.
(SYNT ) SYNTEX USA LLC.
(THOM/) THOMPSON J.
                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-217145/27.
                                                                                                                                                                                     acetylcysteine.
                                                                                                                                                                                                                            WO200211674-A2.
                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                Thompson J,
                                                                                                    02-JUL-2002
                                                                                 ABK59121;
                                                                                                                                                                                                                                                                                                                                                            Grupe A;
                                                    ABK59121
                                           RESULT
                                                                       셤
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The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, chence, are useful for treatment of a patient having a condition acell or sesociated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 where the invention are also used as the presents an examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 where the invention are also used as diagnostic tools to the presence of CLCA1 while sequence represents an enzymatic nucleic acid molecule of the invention

Claim 5; Page 86; 152pp; English.

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                               65.8%; Score 15.8; DB 6; Length 37; 78.9%; Pred. No. 1.46+03; ive 2; Mismatches 2; Indels
Sequence 37 BP; 8 A; 6 C; 16 G; 0 T; 7 U; 0 Other;
                                                                                                 5 GGAGTGATGGCAAGCACGA 23
                                                                                                                   15; Conservative
                                              Best Local Similarity
Matches 15; Conserv
                                      Query Match
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Gaps

15, Conservative

Best Loca Matches

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Human; chloride channel calcium activated 1; CLCA1; 88; antia8thmatic; antiinflammatory; chronic obstructive pulmonary disease, COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Thompson J, Mcswiggen J, Mckenzie T, Ayers D,
                                                                                          Human CLCAl gene enzymatic nucleic acid #3526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 87; 152pp; English.
ABK59155 standard; RNA; 37 BP.
                                                                                                                                                                                                                                                                                                                  09-AUG-2001; 2001WO-US024970.
                                                                                                                                                                                                                                                                                                                                                 09-AUG-2000; 2000US-0224383P.
                                                                                                                                                                                                                                                                                                                                                                                RIBO-) RIBOZYME PHARM INC.
                                                           02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               (SYNT ) SYNTEX USA LLC. (THOM/) THOMPSON J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-217145/27.
                                                                                                                                                                                                                                                     WO200211674-A2
                                                                                                                                                                                        acetylcysteine
                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                 14-FEB-2002.
                               ABK59155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grupe A;
The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving NRA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell, hence, are useful for treatment of a patient having a condition casciated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an
                                                                                                                                                                    Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic; antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37 BP; 10 A; 7 C; 12 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mcswiggen J, Mckenzie T, Ayers D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzymatic nucleic acid molecule of the invention
                                                                                                                                        Human CLCA1 gene enzymatic nucleic acid #3549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 88; 152pp; English.
                                            ABK59178 standard; RNA; 37 BP.
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78.9%;
                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001; 2001WO-US024970
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                                                                                                          02-JUL-2002 (first entry)
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Best Local Similarity 78.37
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           SYNTEX USA LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-217145/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYNT ) SYNTEX USA (THOM/) THOMPSON J.
                                                                                                                                                                                                                                                                                                 WO200211674-A2.
                                                                                                                                                                                                                                      acetylcysteine
                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thompson J,
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                                                                             ABK59178;
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                               ABK59178
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Szymkowski DE;

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The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by clasving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition as useful for treatment of a condition a condition to more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.8; DB 6; Length 37;
Pred. No. 1.4e+03;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 37 BP; 8 A; 5 C; 14 G; 0 T; 10 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enzymatic nucleic acid molecule of the invention
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78.98;
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Matches 15; Conserv
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ABK05394
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AC ABK05:
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Gaps

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Indels

2; Mismatches

GGAGUGAUGGCAUGCACUA 23 5 GGAGTGATGGCAAGCACGA 23

8 a RESULT 37 ABK59155

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12-MAR-2002 (first entry)
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Human NOGO G-Cleaver substrate sequence #57

cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin; e lymphoma; MHL; lymphocytic leukaemia; human immunodeficiency virus; HV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory archropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemocherapy·induced neuropathy; ampotrophic lateral sclerosis; Parkinson's disease; ataxia; Huntington's disease; substrate sequence; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease. Human; 88; antisense therapy; cytostatic; antiinflammatory; haemostatic;

sapiens. Synthetic.

WO200159103-A2

16-AUG-2001

09-FEB-2001; 2001WO-US004273

11-FEB-2000; 2000US-0181797P. 28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P.

RIBOZYME PHARM INC. BLATT L. MCSWIGGEN J. (RIBO-) RIBOZYME PHAR (BLAT/) BLATT L. (MCSW/) MCSWIGGEN J. (CHOW/) CHOWRIRA B M.

Chowrira BM; Mcswiggen J, Blatt L,

WPI; 2001-607195/69.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.

Claim 89; Page 92; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NGGO). The nucleic acids may be enzymatic nucleic acids of eaving a an RNA molecule DNAzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) proposessing an NCH motif). The CD20-targetting nucleic acid is used to cleave RNA with a YCY motif). The CD20-targetting nucleic acid is used to cleave RNA with a YCY motif). The CD20-targetting nucleic acid is used to cleave RNA configuration and treat a patient having a condition associated with the level coff CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-thodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HTV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, cleukaemia, and inflammatory arthropathy. The NOGO gene in the presence of a divalent cation that is preferably Mg²4. Furthermore, the cucleic acid may be contacted with a cell to reduce NOGO activity of the nucleic acid may be contacted with a cell to reduce NOGO activity of the cucleic acid may be contacted with a cell to reduce NOGO activity of the cucleic acid may further comprise the use of one or more characted may further comprise the use of one or more cucleic acid may be contacted with a cell to reduce NOGO activity of the nucleic acid may be contacted with a cell to reduce NOGO activity of the contacted and particular, the NOGO-targetting nucleic acid may be contacted with a cell to reduce NOGO activity of the contacted and may further comprise the use of one or more corrected the nucleic acid may further comprise the use of one or more corrected. The presence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NGGO expression. The present sequence is a substrate sequence for a nucleic acid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The
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                                                                                                                                                                   65.0%; Score 15.6; DB 4; Length 37; 72.7%; Pred. No. 1.8e+03;
                                                                                                                                                                                                       4; Indels
                                                                                                                               Sequence 37 BP; 8 A; 9 C; 12 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human NOGO G-Cleaver substrate sequence #64.
                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                          23
                                                                            sequence is a substrate sequence
based on the human NOGO sequence
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                                                                                                                                                                                                                                             2 AGCGGAGTGATGGCAAGCACGA
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06-MAR-2000; 2000US-0187128P.
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                                                                                                                                                                                                                                                                                                                                                                         ABK05401 standard; RNA; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                  Local Similaricy
nes 16; Conservative
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MCSWIGGEN J.
CHOWRIRA B M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-607195/69.
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Synthetic.
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(MCSW/) N
(CHOW/)
                                                                                                                                                                     Query Match
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cc nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule possessing an NCH motif), a G-leaver (cleaving RNA with an NCH motif) prospessing an NCH motif) proposessing an endologic cleave RNA of CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2</sup> +. C Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more creat lymphoma, laukaemia, HC (Largetting nucleic acid may be used to treat lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic lymphoma, in lymphoma (MLL), immunocytoma (INC), small B-cell lymphocytic lymphoma, immunocytoma (INC), small B-cell lymphocytic lymphocytic lymphoma (INC), small B-cell lymphocytic lymphocytic lymphoma (INC), small B-cell lymphocytic lymphoma, immunocytoma (INC), small B-cell lymphocytic lymp
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65.0%; Score 15.6; DB 4; Length 37; 72.7%; Pred. No. 1.8e+03; Live 2; Mismatches 4; Indels Sequence 37 BP; 11 A; 6 C; 12 G; 0 T; 8 U; 0 Other; Query Match

2 AGCGGAGTGATGGCAAGCACGA 23 2 AGAGAAGUGAUGGCAUGCACUA 23 Best Local Similarity 72.7 Matches 16, Conservative 8

Gaps ć o

> ABK05385 standard; RNA; 37 BP. ABK05385; RESULT 40

Human NOGO G-Cleaver substrate sequence #48. 12-MAR-2002 (first entry)

Human; 88; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCI; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; substrate sequence; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

sapiens. Synthetic.

40200159103-A2

16-AUG-2001

09-FEB-2001; 2001WO-US004273.

The invention relates to a nucleic acid molecule which down regulates expression of a cD20 gene and a nucleic acid molecule which down control of a cD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a numberzyme (an endolytic nucleic acid cleaving RNA with an NCH with a NVH moilf), a G-cleaver (cleaving RNA with an NCH with a NVH woilf) an amberzyme (cleaving RNA with an NGH triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleaver RNA c CC CD20 in the presence of a divalent cation that is preferably Mg^2+.

Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level CC treat lymphoma, leukemia, be coll lymphoma, ucleic acid may be used to therapise. In particular, the CD20 targetting nucleic acid may be used to cleave the use of one or more condition and (NHL), bulky low-grade or follicular NHL, lymphocytic lymphoma (NLL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, in the contacted with a cell in to reduce NOGO gene in the content of a divalent cation that is preferably Mg^2+. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the content of a divalent cation that is preferably Mg^2+. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the contact of a divalent and inflammatory arthropathy. The NOGO created may be contacted with a cell to reduce NOGO activity of the contact central nervous system (NNS) injury and created with the level of themotherapy-induced neuropathy, and/or other moules acid may be used to cleave, Alzheimer's disease, disease, muscular dystrophy, and/or other neurodegenerative disease tracks, Huntington's disease, central nervous system (NNS) injury and created solve of the endormal nervous system (NNS) injury and created solve of the endormal nervous Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and Sequence 37 BP; 5 A; 7 C; 20 G; 0 T; 5 U; 0 Other; Chowrira BM; Claim 89; Page 92; 200pp; English. based on the human NOGO sequence central nervous system injury. 11-FEB-2000; 2000US-0181797P. 28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P. RIBOZYME PHARM INC Blatt L, Mcswiggen J, CHOWRIRA B M. MCSWIGGEN J. WPI; 2001-607195/69. BLATT L. (RIBO-) (BLAT/) (CHOM/) (MCSM/)

Gaps ö Ouery Match 65.0%; Score 15.6; DB 4; Length 37; Best Local Similarity 72.7%; Pred. No. 1.8e+03; 4; Indels 2; Mismatches 16; Conservative

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Search completed: December 13, 2005, 13:34:14 Job time : 370.5 secs

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OM nucleic

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Sequence:

Searched:

Database

Result No.

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Pasha, A.Q. and Ahsan, A.
Method of detecting predisposition to high altitude pulmonary edema
Patent: WO 200547540-A 2 26-MAY-2005;
Council of Scientific and Industrial Research (IN)
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AX219959 6
AR335309 6
AR336709 6
AR336775 8
AR43656 6
AR436756 6
AX220062 7
AX220022 6
AX220022 6
AX220010 6
AX22010 6
AX22010
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/organism="synthetic construct"
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other sequences; artificial sequences
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Sequence 5395 from Patent WO0159103.
AX219953
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Sequence 2 from Patent WO2005047540.
CS101222
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 AX219959
AR335309
AR335309
AR335735
AR336775
AR336775
AR436566
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AX228845
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AX22820
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AX228569
                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E. and Grupe, A. Mcthod and reagent for the inhibition of calcium activated chloride channel—1 (clca-1)
Patent: WO 0211674-A 3502 14-FEB-2002;
RIBOZYME PHARMACEUTCALS, INC. (US); Syntex (U.S.A.) LLC (US);
Thompson, James (US)
Location/Qualifiers
                                                                                                                                                                                                                                                  Query Match 69.2%; Score 16.6; DB 6; Length 37; Best Local Similarity 82.6%; Pred. No. 1.1e+04; Matches 19; Conservative 0; Mismatches 4; Indels
McSwiggen, James (US); Chowrira, Bharat M. Location/Qualifiers
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/mol_type="unassigned RNA"
/bxref="taxon:32630"
/noTe="Enzymatic Nucleic Acid"
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/mol_type="unassigned RNA"
/mol_type="taxon:32630"
/nofe="Nucleic Acid"
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AX581664.1 GI:27653474
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AX219924.1 GI:15547648
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                                                 Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0151913-A 5395 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Patent: WO 0159103-A 5358 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US)
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Method and reagent for the modulation and diagnosis
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/db_xref="taxon:32630"
/note="Nucleic Acid"
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Indels

Length 37;

PAT 07-SEP-2001

linear

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Lawrence (US)

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PAT 07-SEP-2001
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 13000 20-MAY-2003;
Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
Ribozyme Location/Qualifiers
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Unclassified.
1 (bases 1 to 36)
Eckstein,F., Ludwig,J. and Beigelman,L.
Eckstein,F., Ludwigts with endonuclease activity
Nucleic acid catalysts with endonuclease activity
Patent: US 6656731-A 597 02-DEC-2003;
Patent: US 6656731-A 597 nor-bec-2003;
Sirna Therapeutics; Munich;
DEX;
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89.5%; Pred. No. 2.6e+04;
iive 0; Mismatches 2;
                                                                                                        Sequence 13000 from patent US 6566127. AR135598
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AR436338.1 GI:40199422
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Sequence 5427 from Patent WO0159103.
AX219985
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/mol_type="unassigned RNA"
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/wol_type="unassigned RNA"
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AR436338
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AX219985
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Method and reagent for the inhibition of erg
Patent: WO 018B124-A 3368 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Pavoc, P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Bavoc,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 12979 20-MAY-2003;
Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, Clocation/Qualifiers
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                                                                                 Score 16.2; DB 6;
Pred. No. 1.7e+04;
0; Mismatches 3;
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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Sequence 12979 from patent US 6566127.
AR335577
AR335577.1 GI:33721385
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synthetic construct
other sequences; artificial sequences.
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Sequence 3368 from Patent WO0188124.
AX425032
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/wol_type="unassigned RNA"
 /mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
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Best Local Similarity 85.73
Matches 18; Conservative
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Best Local Similarity 85.7
Matches 18; Conservative
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                                                                                    Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0153103-A 5427 16-AUG-2001;
RIBOXYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Describesion
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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/organism="synthetic construct"
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/noTe="Nucleic Acid"
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="teaxon:32630"
/noTe="Nucleic Acid"
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                                                           other sequences; artificial sequences.
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other sequences; artificial sequences.
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    AX219985.1 GI:15547709
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AUTHORS
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AX223033
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Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
Patent: WO 0211674-A 3492 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US);
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Fattaey, A.R., Jarvis, T., Mcswiggen, J., Booher, R.N. and Holman, P.S. Method and reagent for the inhibition of checkpoint kinase-1 (chk 1) enzyme WO 0157206-A 1927 09-AUG-2001; RIBOZYME PHARMACEUTICALS, INC. (US); Fattaey, Ali R. (US) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E.
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65.8%; Score 15.8; DB 6;
Best Local Similarity 89.5%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 2;
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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/mol_type="unassigned RNA"
/db xref="teaxon:32630"
/noTe="Enzymatic Nucleic Acid"
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other sequences; artificial sequences.
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other sequences; artificial sequences.
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Sequence 3492 from Patent W00211674..
AX581654
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Location/Qualifiers
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PAT 07-SEP-2001
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
patent: WO 0159103-A 5401 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 5394 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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                                                                                                       Length 37;
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81.8%; Pred. No. 3.2e+04;
:ive 0; Mismatches 4;
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/organism="synthetic construct"
/mol_type="unassigned RNA"
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/noTe="Nucleic Acid"
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/noTe="Nucleic Acid"
/organism="synthetic construct"
/mol type="unassigned RNA"
/mol type="taxon:3260"
/note="Nucleic Acid"
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Sequence 5394 from Patent W00159103.
AX219952
AX219952.1 GI:15547676
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Patent: WO 0211674-A 3549 14-FEB-2002;
RIBOZYME PHARMACEUTCALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 5385 16-AUG-2001;
RIBOZYME HARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
 RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US)
Thompson, James (US)
Location/Qualifiers
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89.5%; Pred. No. 2.6e+04;
ive 0; Mismatches 2; Indels
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Pred. No. 2.6e+04;
0; Mismatches 2;
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon.32630"
/noFe="Enzymatic Nucleic Acid"
                                                         1.37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="reaxon:32630"
/note="Enzymatic Nucleic Acid"
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Sequence 5385 from Patent W00159103.
AX219943.1 GI:15547667
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Sequence 3549 from Patent WO0211674.
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Location/Qualifiers
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Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                                  Unclassified.

1 (bases 1 to 36)
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 14177 20-MAY-2003;
Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
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Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 14200 20-MAY-2003;
Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
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Pred. No. 4.9e+04;
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Eckstein,F., Ludwig,J. and Beigelman,L.
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   AR336775 36 bp RNA
Seguence 14177 from patent US 6566127.
AR336775
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Sequence 14200 from patent US 6566127.
AR336798
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Sequence 825 from patent US 6656731.
AR436566.1 GI:40199650

    .36
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Unclassified.
1 (Dases I to 36)
1 (Dases I to 36)
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Rethod and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 12725 20-MAY-2003;
Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
Location/Qualifiers
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   Length 37;
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                                   4; Indels
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Query Match 65.0%; Score 15.6; DB 6; Best Local Similarity 81.8%; Pred. No. 3.2e+04; Matches 18; Conservative 0; Mismatches 4;
                                                                                                                                                                              36 bp RNA
Sequence 12711 from patent US 6566127.
AR335309.1 GI:33721117
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Sequence 12725 from patent US 6566127.
AR335323
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                                                                  2 AGCGGAGTGATGGCAAGCACGA 23
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 5367 16-AUG-2001;
RIBOZYME PHARMACEUTIAALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Method and reagent for the modulation and diagnosis of cd2(
nogo gene expression
Patent: WO 0159103-A 5504 16-AUG-2001;
RIBOZYME PHARMACEUTICAS, INC. (US); Blatt, Lawrence (US)
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Pred. No. 4.9e+04;
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Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3;
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="texon:32630"
/noTe="Nucleic Acid"
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/mol type="unassigned RNA"
/db_xref="taxon:32630"
/nofe="Nucleic Acid"
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Sequence 5504 from Patent WO0159103.
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Sequence 5367 from Patent WO0159103.
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     /db_xref="taxon:32630"
/note="Nucleic Acid"
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Unclassified.
Lobasea 1 to 36)
Eckstein,F., Ludwig,J. and Beigelman,L.
Nucleic acid catalysts with endonuclease activity
Patent: US 6565731-A 1014 02-DEC-2003;
Max Planck Gesellschaft zur Forderung der Wissenschaften E.V. and Sirna Therapeutics; Munich;
Nucleic acid catalysts with endonuclease activity
Patent: US 6656731-A 825 02-DEC-2003;
Max Planck Gesellschaft zur Forderung der Wissenschaften E.V. and
Sirna Therapeutics; Munich;
DEX;
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0153103-A 5364 16-AUG-2001;
RIBOXYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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63.3%; Score 15.2; DB 6;
Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3;
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/mol_type="unassigned RNA"
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AR436755
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Sequence 5364 from Patent W00159103.
AX219922
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/organism="unknown"
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AR436755
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PAT 18-JUN-2002

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Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E. and Grupe, A. Method and reagent for the inhibition of calcium activated chloride channel—I (clca—1)
Patent: WO 0211674-A 3453 14-FEB-2002;
RIBOZYME PHARMACEUTCALS, INC. (US); Syntex (U.S.A.) LLC (US);
Thompson, James (US)
Location/Qualifiers
                                                                                                                                                                         Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Mclaughlin, F.G. and Randi, A.M.
Method and reagent for the inhibition of erg
Patent: WO 0188124-A 328 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.3%; Score 15.2; DB 6; Length 37; Best Local Similarity 85.0%; Pred. No. 4.9e+04; Matches 17; Conservative 0; Mismatches 3; Indels
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other sequences; artificial sequences.
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Sequence 3453 from Patent WO0211674.
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AX581615.1 GI:27653425
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                     37 bp RN Sequence 3288 from Patent WO0188124.
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Patent: WO 0157206-A 1894 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
Location/Qualifiers
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Patent: WO 0157206-A 1917 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
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/db_xref="taxon:32630"
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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AX228522
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Sequence 1917 from Patent WO0157206.
AX228545 AX228545.1 GI:15557686
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 5553 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 5453 16-AUG-2001;
RIBOZYME WO 0159103 5 16-AUG-2001;
MCSWiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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/bb xref="taxon:32630"
/note="Nucleic Acid"
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/mol_type="unassigned RNA"
/bo xref="taxon.32630"
/note="Nucleic Acid"
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Sequence 5542 from Patent WO0159103.
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AX220100.1 GI:15547824
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0153103-A 5352 16-AUG-2001;
RIBOXYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
                                                                                            Blatt,L., Mcswiggen,J. and Chowrira,B.M. Method and reagent for the modulation and diagnosis of cd20 and
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Patent: WO 0159103-A 5339 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US)
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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Pred. No. 6.1e+04;
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/hb xref="taxon:32630"
/noTe="Nucleic Acid"
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Sequence 5352 from Patent WO0159103.
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Search completed: December 13, 2005, 14:11:38 Job time : 1118.5 secs
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Matches 18; Conservative
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AUTHORS
TITLE
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AX228610
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0153103-A 5562 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
                                                                                                                                                                                                                                                                                                                                         Gaps
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, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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/organisme="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="texon:32630"
/note="Nucleic Acid"
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db xref="texon:32630"
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Sequence 1981 from Patent WO0157206.
AX228609
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Sequence 5562 from Patent WO0159103.
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Best Local Similarity 78.3<sup>3</sup>
Matches 18; Conservative
      McSwiggen,
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DEFINITION
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AX228609
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Patent: WO 0157206-A 1982 09-AUG-2001;
RIBOZYWE PHARMACEUTICALS, INC. (US); Fattaey, Ali R. (US)
Location/Qualifiers
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62.5%; Score 15; DB 6; Length 37; 78.3%; Pred. No. 6.1e+04;
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                                             5; Indels

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    forganism="synthetic construct"
|mol type="unassigned RNA"
|db_xref="taxon:32630"

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Sequence 1982 from Patent WO0157206.
AX228610
                                          0; Mismatches
                                                                                     1 CAGCGGAGTGATGCCACGA 23
                                                                                                                1 CATAGCAGTGATGGCATGCACTA 23
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Sequence 1526049, Sequence 152926, Sequence 92175, A Sequence 1302115, Sequence 1313799, Sequence 1313893, Sequence 1313893,

92175, A 624295, 1302115, 1313799,

387902, 503486, 387702, 387807, 387902, 503486,

Sequence Sequence Sequence Sequence Sequence Sequence 1345869,

1313893,

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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Run on:

Sequence:

Searched:

Database

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61.7%; Score 14.8; DB 8; Length 19; 77.8%; Pred. No. 4.1e+02; ive 2; Mismatches 2; Indels
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APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Laake, Devin
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
SPRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 253506
US-11-101-244-387807

US-11-101-244-387902

US-11-101-244-387902

US-11-083-784-387902

US-11-083-784-387902

US-11-083-784-503486

US-11-101-244-92175

US-11-101-244-1313893

US-11-101-244-1313893

US-11-101-244-1313893

US-11-101-244-1313893

US-11-101-244-1345869

US-11-083-784-622926

US-11-083-784-622926

US-11-083-784-132926

US-11-083-784-132926

US-11-083-784-13799

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US-11-083-784-131399

US-11-083-784-131399
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Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Rhyorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Rese, Devin
APPLICANT: Marshall, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 253506, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
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; ORGANISM: Homo sapiens
US-11-101-244-253506
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US-11-101-244-253506
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Sequence 639666,
Sequence 940716,
Sequence 987947,
Sequence 253501,
Sequence 422572,
Sequence 422581,
Sequence 639666,
Sequence 940716,
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Sequence 36, Appl
Sequence 314817,
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Sequence 314817,
Sequence 253501,
Sequence 452572,
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41.830 Million cell updates/sec
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| Cgn2_6 | ptodata/2/pubpna/USO6_NEW_PUB.seq:*
| Cgn2_6 | ptodata/2/pubpna/USO6_NEW_PUB.seq:*
| Cgn2_6 | ptodata/2/pubpna/USO8_NEW_PUB.seq:*
| Cgn2_6 | ptodata/2/pubpna/DSO7_NEW_PUB.seq:*
| Cgn2_6 | ptodata/2/pubpna/USO8_NEW_PUB.seq:*
| Cgn2_6 | ptodata/2/pubpna/USO8_NEW_PUB.seq:*
| Cgn2_6 | ptodata/2/pubpna/USO8_NEW_PUB.seq:*
| Cgn2_6 | ptodata/2/pubpna/USO8_NEW_PUB.seq:*
| Cgn2_6 | ptodata/2/pubpna/USO8_NEW_PUB.seq3:*
| Cgn2_6 | ptodata/2/pubpna/USO8_NEW_PUB.seq3:*
| Cgn2_6 | ptodata/2/pubpna/USO8_NEW_PUB.seq3:*
                               GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-11-003-784-253506
US-11-003-784-126494
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US-10-1003-784-126494
US-11-101-244-253501
US-11-101-244-452572
US-11-101-244-452572
US-11-101-244-452572
US-11-101-244-950716
US-11-101-244-940716
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US-11-103-784-253501
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US-11-003-784-639666
US-11-003-784-940716
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Maximum Match 100%
Listing first 45 summaries
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Match Length
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Maximum DB seq length: 50
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Result

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Sequence 36, Application US/10508932

Sequence 36, Application US/10508932

Publication No. US20050260586A1

GENERAL INFORMATION:
APPLICANT: Weaver, David A.
APPLICANT: Weaver, David A.
APPLICANT: Weaver, Timothy G.
APPLICANT: Crawford, Erin L.
APPLICANT: Crawford, Erin L.
TITLE OF INVENTION: Method and Compositions for the Diagnosis and Treatment of Non-S.
TITLE OF INVENTION: Lung Cancer Using Gene Expression Profiles
FILE REPERENCE: 9050

CURRENT APPLICATION NUMBER: US/10/508,932

CURRENT FILING DATE: 2004-09-24

NUMBER OF SEQ ID NOS: 48

SEQ ID NOS: 48

SEQ ID NO 36

LUNCH OF THE NO 36

SEQ ID NO 36
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  APPLICANT: Marshall, William APPLICANT: Scaringe, Stephen TITLE OF INVENTION: Functional and Hyperfunctional siRNA FIE REFERENCE: 13499US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 60.0%; Score 14.4; DB 9; Best Local Similarity 87.5%; Pred. No. 6.2e+02; Matches 14; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14.4; DB 6;
Pred. No. 6.3e+02;
0; Mismatches 6;
                                                                                    CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 GATGAGAGGGGGGACCAAGAAG 14
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Reynolds, Angela
Leake, Devin
Marshall, William
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-508-932-36
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US-11-083-784-126494
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Best Local Similarity
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APPLICANT:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 125.4594, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Eake, Devin
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respendin, William
APPLICANT: Marehall, William
APPLICANT: Marehall, William
APPLICANT: Marehall, William
APPLICANT: Boaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT PILING DATE: 2005-00-07
PRIOR PLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/126,137
PRIOR APPLICATION NUMBER: 60/126,137
PRIOR PLICATION NUMBER: 2002-11-14
SOFTWARE: PEOPILEATOR
SEQ ID NOS: 1591911
SEQ ID NO 126494
HAPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349908
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR FILING DATE: 2005-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFUMBER: PROPILEATION NUMBER: 60/426,137
SEQ ID NOS: 1591911
SOFUMBER: PROPILEATY
SEQ ID NOS: 1591911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.7%; Score 14.8; DB 9; 77.8%; Pred. No. 4.1e+02;
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; Sequence 126494, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khyorova, Anastasia
; APPLICANT: Leake, Devin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TGCACAGCTGGGGAACAA 20
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Best Local Similarity 77.8 Marches 14; Conservative
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US-11-101-244-126494
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US-11-083-784-253506
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| GENERAL INFORMATION: |
| APPLICANT: Dharmacon, Inc. |
| APPLICANT: Rhvorova, Anastasia |
| APPLICANT: Reynolds, Angela |
| APPLICANT: Reynolds, Angela |
| APPLICANT: Marshall, William |
| APPLICANT: Scarings, Stephen |
| TITLE OF INVENTION: Functional and Hyperfunctional siRNA |
| FILE REFERENCE: 13499US |
| CURRENT APPLICATION NUMBER: US/11/101,244 |
| CURRENT FILING DATE: 2003-09-10 |
| PRIOR PILIONG DATE: 2003-09-10 |
| PRIOR PLICATION NUMBER: 60/426,137 |
| PRIOR PLICATION NUMBER: 60/426,137 |
| PRIOR PLICATION NUMBER: 60/426,137 |
| SOFTWARE: PROPRIECATY |
| SOFTWARE: PROPRIECATY |
| SOFTWARE: PROPRIECATY |
| LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 19;
                  APPLICANT: Catalinge, Stephen;
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA;
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR PILING DATE: 2005-04-07
PRIOR PLILING DATE: 2002-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 253501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 57.5%; Score 13.8; DB 8; Best Local Similarity 82.4%; Pred. No. 1.2e+03; Matches 14; Conservative 1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 452572, Application US/11101244; Publication No. US20050246794A1
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APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GCACAGCTGGGGAACAA 20
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-11-101-244-253501
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Best Local Similarity
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Pred. No. 7.6e+02;
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APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPREMENT 34990H
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
## APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILLS REFERENCE: 13499US

CURRENT APPLICATION WUMBER: US/11/101,244

CURRENT FILING DATE: 2005-04-07

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR PILING DATE: 2003-09-10

PRIOR PILING DATE: 2003-09-10

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTHARE: Proprietary

SEQ ID NO 314817

LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.2; DB 9;
Pred. No. 7.6e+02;
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; GENERAL INFORMATTON:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khovorova, Anastasia
APPLICANT: Khovorova, Anastasia
APPLICANT: Leake, Devin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 314817, Application US/11083784 Publication No. US20050245475A1 GENERAL INFORMATION:
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Best Local Similarity 78.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                59.2%;
78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 78.9
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens US-11-083-784-314817
                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-11-101-244-314817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-083-784-314817
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US-11-101-244-940758
US-11-101-244-940758
Sequence 940758, Application US/11101244
Publication No. USC0050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynoids, Angela
APPLICANT: Reynoids, Angela
APPLICANT: Beake, Devin
APPLICANT: Beake, Devin
APPLICANT: Beake, Devin
APPLICANT: Beake, Devin
APPLICANT: Leake, Devin
APPLICANT: Anterional and Hyperfunctional siRNA
ITILE OF INVENTION: Functional and Hyperfunctional
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-11
SOFTWARE: Proprietary
SOFTWARE: Proprietary
INVENT: PILNG DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 19;
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APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.5%; Score 13.8; DB 8; B2.4%; Pred. No. 1.2e+03; Long. No. 1.2e+04; Long. No. 1.2e+03; Long. No. 1.2e+04; Long. No. 1.2e+04; Long. No. 1.2e+04; Long. No. 1.2e+04; Long. No. 1.2e+06; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                  FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR PELICATION NUMBER: 60/502,050
PRIOR PELICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-09-10
PRIOR PELICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SOFTWARE: 100 NO 940716
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Best Local Similarity 82.4<sup>a</sup>
Matches 14<sup>a</sup>, Conservative
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; ORGANISM: Homo sapiens
US-11-101-244-940758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-11-101-244-940716
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Best Local Similarity
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US-11-101-244-987947
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
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Pred. No. 1.2e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 639666, Application US/11101244
; Bublication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.;
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Respect bearing, Applicant: Reynolds, Angela
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; APPLICANT: Narshall, William
; APPLICANT: Narshall, William
; APPLICANT: Narshall, William
; APPLICANT: WILL Beake, Scephen
; TILE REFERENCE: 13499U8
; CURRENT FILING DATE: 2003-04-07
; PRIOR PLICATION NUMBER: 60/426,137
; PRIOR PLICATION NUMBER: 60/426,137
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SGO ID NO 639666
LENGTH: 19
       HAPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILLS REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
FRIOR FILING DATE: 2005-04-07
FRIOR PLILING DATE: 2003-09-10
FRIOR PLILING DATE: 2003-09-10
FRIOR FILING DATE: 2003-09-10
FRIOR FILING DATE: 2003-09-10
SROID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 452581
LENGTH: 19
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Sequence 940716, Application US/11101244

PUDLication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
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Reynolds, Angela
Leake, Devin
Marshall, William
Scaringe, Stephen
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Best Local Similarity 76.5
Matches 13; Conservative
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US-11-101-244-639666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-452581
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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; Publication No. US20050245475A1
; GENERAL INFORMATION:
    APPLICANT: Dharmacon, Inc.
; APPLICANT: Revoolds, Ansetasia
; APPLICANT: Revoolds, Ansetasia
; APPLICANT: Revoolds, Ansetasia
; APPLICANT: Leake Devin
; APPLICANT: Leake Devin
; APPLICANT: Scaringe, Stephen
; TILLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349908;
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR APPLICATION NUMBER: 60/426,137
; RIOR APPLICATION NUMBER: 60/426,137
; ROFTWARE: PROPRIET 2002-11-14
; SEOTHWARE: PROPRIET 2002-11-14
; SOFTWARE: PROPRIET 2002-11-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.5%; Score 13.8; DB 9;
82.4%; Pred. No. 1.2e+03;
tive 1; Mismatches 2;
                          FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT APLICATION NUMBER: US/10/714,333
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR PLILNG DATE: 2003-11-14
PRIOR PLILNG DATE: 2003-09-10
PRIOR PLILNG DATE: 2003-11-14
PRIOR PLILNG DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
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Sequence 639666, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Rhyorova, Anastasia
APPLICANT: Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GCACAGCTGGGGAACAA 20
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Best Local Similarity 82.3.
Best Local 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 82.49
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-452572
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US-11-083-784-452581
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sequence 253501, Application US/11083784
publication No. U320050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.;
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respect Reynolds, Angela
APPLICANT: Respect 
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                          CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 997947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 452572, Application US/11083784 Publication No. US20050245475A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ACAGCUGGGUAAUAAGA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GCACAGCTGGGGAACAA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 82.48
Matches 14; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                      ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-987947
      FILE REFERENCE: 13499US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-11-083-784-452572
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RESULT 21
US-11-083-784-987947
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US-11-083-784-940716
i Sequence 940716, Application US/11083784
i Sequence 940716, Application US/11083784
i Sequence 940716, Application US/11083784
i GENERAL INFORMATION:
i APPLICANT: Khyorova, Ansetasia
APPLICANT: Khyorova, Ansetasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: More Encional and Hyperfunctional siRNA
FILE OF INVENTION: Functional and Hyperfunctional
FURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
FRIOR FILING DATE: 2003-11-14
FRIOR FILING DATE: 2003-11-14
FRIOR FILING DATE: 2003-11-14
SRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARRE: POPPLICATY
SEQ ID NO 940716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 19;
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVERTON: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PLING DATE: 2005-03-18
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 639666
LENGTH: 19
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57.5%; Score 13.8; DB 9;
Best Local Similarity 76.5%; Pred. No. 1.2e+03;
Matches 13; Conservative 2; Mismatches 2;
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US-11-083-784-940716
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-11-083-784-639666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-083-784-940758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 987947, Application US/11083784
; Publication No. US20050245475A1
; GREREAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Resynolds, Angela
; APPLICANT: Scaringe, Stephen
; APPLICANT: Scaringe, Stephen
; TITLE OP INVENTION: Functional and Hyperfunctional siRNA
; TILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083, 784
; CURRENT PLING DATE: 2003-118
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR APPLICATION NUMBER: 60/426,137
; RIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; RIOR PLING DATE: 2003-09-10
; RIOR PLING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1591911
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                                        APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTON: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2005-03-18
PRIOR PILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-10-10
PRIOR FILING DATE: 2003-10-10
PRIOR FILING DATE: 2003-10-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 940758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 57.5%; Score 13.8; DB 9; Best Local Similarity 82.4%; Pred. No. 1.2e+03; Matches 14; Conservative 1; Mismatches 2;
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Anastasia
                          Angela
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Best Local Similarity 82.4<sup>†</sup>
Matches 14; Conservative
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US-11-083-784-987947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-11-083-784-940758
     Khvorova,
Reynolds,
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RESULT 22 US-10-770-726-10883/c

; Sequence 940758, Application US/11083784; Publication No. US20050245475A1; GENERAL INFORMATION:

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Pred. No. 1.7e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 387902.
Sequence 387902. Application US/11101244
Fublication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Whorova, Inc.
APPLICANT: Rhorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Beake, Devin
APPLICANT: Booton Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349908.
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 387902.
LENGTH. 10
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 55.8%; Score 13.4; DB 8; Length 19; Best Local Similarity 86.7%; Pred. No. 1.7e+03; Matches 13; Conservative 1; Mismatches 1; Indels
               APPLICANT: Scaringe, Stephen; TITLE OF INVENTION: Functional and Hyperfunctional siRNA; FILE REFERENCE: 1349908; CURRENT APPLICATION NUMBER: US/11/101,244; CURRENT FILING DATE: 2005-04-07; PRIOR APPLICATION NUMBER: 60/502,050; PRIOR APPLICATION NUMBER: 60/426,137; PRIOR APPLICATION NUMBER: 60/426,137; PRIOR PILING DATE: 2002-11-14; NUMBER OF SEQ ID NOS: 1591911; SOFTWARE: Proprietary; SEQ ID NO 397807.
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; Publication No. US20050246794A1
; GENERAL INFORMATION:
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reprolda, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.8%;
86.7%;
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Best Local Similarity 86.7"
....hes 13; Conservative
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US-11-101-244-387902
                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-387807
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US-11-101-244-503486
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US-11-101-244-387902
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                                                                                          APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT APPLICATION NUMBER: US/204-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 56.7%; Score 13.6; DB 6; Length 21; Best Local Similarity 80.0%; Pred. No. 1.4e+03; Matches 16; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Sequence 387702, Application US/11101244
| Publication No. US20050346794A1
| GENERAL INFORMATION:
| APPLICANT: Inharmacon, Inc.;
| APPLICANT: Rhyorova, Anastasia
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Marshall, William
| APPLICANT: Marshall, William
| APPLICANT: Scaringe, Stephen
| TITLE OF INVENTION: Functional and Hyperfunctional siRNA
| FILE REPERENCE: 13499US
| CURRENT APPLICATION NUMBER: 60/502.050
| PRIOR FILING DATE: 2005-09-10
| PRIOR PPLICATION NUMBER: 60/426,137
| PRIOR PLING DATE: 2002-11-14
| NUMBER OF SEQ ID NOS: 1591911
| SOFTWARE: Proprietary
| LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
Sequence 10883, Application US/10770726
Publication No. US20050266409A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TGCACAGCTGGGGAACAAGA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 rccacagcrgrggaaraara 1
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                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
GORGANISM: Homo sapiens
US-10-770-726-10883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-11-101-244-387702
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                                                                              APPLICANT: Wyeth
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Sequence 387902
; Sequence 387902, Application US/11083784
; Publication No. US2050245475A1
; GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Beynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Beynolds, Miliam
APPLICANT: Bennell, William
APPLICANT: Bearling Stephen
CURRENT MAPLICATION WUMBER: US/11/083,784
CURRENT APPLICATION NUMBER: US/11/4,333
FRIOR PILING DATE: 2005-01-18
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR PILING DATE: 2003-09-10
FRIOR PILING DATE: 2003-09-10
FRIOR PILING DATE: 2003-11-14
FRIOR PILING DATE: 2003-11-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 19;
                        APPLICANT: Scatinge, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR PILING DATE: 2005-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 55.8%; Score 13.4; DB 9; Best Local Similarity 86.7%; Pred. No. 1.7e+03; Matches 13; Conservative 1; Mismatches 1;
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US-11-083-784-503486
; Sequence 503486, Application US/11083784
; Publicatlon No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACAGCUGGUGAACA 18
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Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-11-083-784-387807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-083-784-387902
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; Sequence 387702, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
    APPLICANT: Dharmacon, Inc.; APPLICANT: Revolds, Ansatasia
    APPLICANT: Revolds, Ansatasia
    APPLICANT: Revolds, Ansatasia
    APPLICANT: Revolds, Ansatasia
    APPLICANT: Beake, Devin
    APPLICANT: Beake, Devin
    APPLICANT: Scaringe, Stephen
    TITLE OF INVENTION: Functional and Hyperfunctional siRNA
    FILE REPREARCE: 13499US: US/11/083,784
    CURRENT APPLICATION NUMBER: US/11/083,784
    CURRENT PILING DATE: 2005-03-18
    PRIOR APPLICATION NUMBER: G0/502,050
    PRIOR FILING DATE: 2003-11-14
    PRIOR FILING DATE: 2003-09-10
    PRIOR FILING DATE: 2003-11-14
    PRIOR FILING DATE: 2002-11-14
    NUMBER OF SEQ ID NOS: 1591911
    SOFTWARE: Proprietary
    LENGTH: 19702
    LENGTH: 19702
    LENGTH: 19702
    LENGTH: 19702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.4; DB 8; Length 19;
Pred. No. 1.7e+03;
2; Mismatches 1; Indels
## APPLICANT: Scaringe, Stephen
| TITLE OF INVENTION: Functional and Hyperfunctional siRNA |
| FILE REFERENCE: 1499US |
| CURRENT APPLICATION NUMBER: US/11/101,244 |
| CURRENT FILING DATE: 2005-04-07 |
| PRIOR APPLICATION NUMBER: 60/502,050 |
| PRIOR PILING DATE: 2003-09-10 |
| PRIOR PILING DATE: 2003-09-10 |
| PRIOR PILING DATE: 2003-09-10 |
| STOR FILING DATE: 2003-11-14 |
| NUMBER OF SEQ ID NOS: 1591911 |
| SOFTWARE: Proprietary |
| LENGTH: 19
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Sequence 387807, Application US/11083784

PUBLICATION NO. USSO050245475A1

SENERAL INFORMATION:

APPLICANT: Bharmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.8%;
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Best Local Similarity 80.01
Matches 12; Conservative
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US-11-083-784-387702
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-503486
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55.0%; Score 13.2; DB 8; Length 19; 72.2%; Pred. No. 2.2e+03;
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                                     APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Acaringe, Stephen
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 624295
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Khorova, Anaetasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13490US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
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Pred. No. 2.2e+03;
2; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1302115, Application US/11101244; Publication No. US20050246794A1; GENERAL INFORMATION:
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Khvorova, Anastasia
Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.0%;
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SOFTWARE: Proprietary
SEQ ID NO 1302115
LENGTH: 19
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Best Local Similarity 72.2
Matches 13; Conservative
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Homo sapiens
US-11-101-244-624295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 33
US-11-101-244-1302115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-101-244-1313799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.8%; Score 13.4; DB 9; Length 19; 80.0%; Pred. No. 1.7e+03; Live 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 92175, Application US/11101244
publication No. US200S0246794A1
GENERAL INPORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respect Devin
APPLICANT: Responds, Angela
APPLICANT: Barahll, William
APPLICANT: Marahll, William
APPLICANT: Boringe, Stephen
TILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 134990S
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
                 APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-01-10
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-10-10
PRIOR FILING DATE: 2003-11-14
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SOFTWARE: Proprietary
SEQ ID NO 503486
LENGTH: 19
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     Angela
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-11-083-784-503486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 12; Conserv
  Reynolds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 31
US-11-101-244-92175/c
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US-11-101-244-624295
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Sequence 1526049, Application US/11101244; Publication No. US20050246794A1; GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc., APPLICANT: Reynolds, Angela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 CACAGCTGGGGAACAAGA 22
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    Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 77.85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-11-101-244-1360531
                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-11-101-244-1345869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 37
US-11-101-244-1360531
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 13.2; DB 8; Length 19;
Pred. No. 2.2e+03;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 13.2; DB 8; Length 19;
Pred. No. 2.2e+03;
2; Mismatches 3; Indels
            APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFREENCE: 134990US
CURRENT APPLICATION NUMBER: 06/502,050
PRIOR FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SQOTWARE: Proprietary
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dharmacon, Inc.
APPLICANT: Characon, Inc.
APPLICANT: Rhvorova, Anastasia
APPLICANT: Leake, Devin
APPLICANT: Marshall, Milliam
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR PLING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1313893
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1313893, Application US/11101244 Publication No. US20050246794A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1345869, Application US/11101244; Publication No. US20050246794A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 TGCACAGCTGGGGAACAA 20
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Khvorova, Anastasia
Reynolds, Angela
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APPLICANT: Khvorova, Anastasia
                                                                                                                                                                                                                                                                                                                                                                                                                                      55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
CNGANISM: Homo sapiens
US-11-101-244-1313799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-11-101-244-1313893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 19;
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephner
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SCPTWARE: PROPRIETE: 2002-11-14
SEQ ID NO 1345869
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dharmacon, Inc.
APPLICANT: Dharmacon, Anaetasia
APPLICANT: Reynolds, Angela
APPLICANT: Resynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Resynolds, Angela
APPLICANT: Resynolds, Angela
APPLICANT: Resynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1360531
LEWARTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 55.0%; Score 13.2; DB 8; Best Local Similarity 77.8%; Pred. No. 2.2e+03; Matches 14; Conservative 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1360531, Application US/11101244; Publication No. US20050246794A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.0%; Score 13.2; DB 8; Length 19; 72.2%; Pred. No. 2.2e+03; Live 2; Mismatches 3; Indels
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR PLING DATE: 2003-09-10
PRIOR PLING DATE: 2003-09-10
PRIOR PLING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
SROR RED SEQ ID NOS: 1591911
SOFTWARE: PROPRIETARY
SEQ ID NO 1526049
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Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Charmacon, Inc.
APPLICANT: Rivorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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Sequence 92175, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: KIVOROVA, Anastasia

APPLICANT: Reynolds, Angela
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Best Local Similarity 72.21
Best Local 3; Conservative
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US-11-101-244-1529226
                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1526049
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US-11-101-244-1529226
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### APPLICANT: Scaringe, Stephen
### TILE OF INVENTION: Functional and Hyperfunctional siRNA
### FILE OF INVENTION: Functional and Hyperfunctional siRNA
### CURRENT APPLICATION NUMBER: US/11/083,784
### CURRENT FILING DATE: 2003-03-18
### PRIOR PILING DATE: 2003-11-14
### PRIOR PILING DATE: 2002-11-14
### PRIOR PILING DATE: 2005-11-14
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